

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 07:19:47 ; Search time 10.1722 Seconds
(without alignments)
151.341 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 OKRAVDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	376	1 RHECDJ	heat shock protein
2	86	100.0	376	2 G90630	DnaJ protein [impo
3	86	100.0	376	2 G85481	chaperone with dna
4	86	100.0	379	2 AF0503	DnaJ protein [impo
5	86	100.0	379	2 AB0058	chaperone protein
6	86	100.0	394	2 C64112	heat shock protein
7	83	96.5	381	2 D82270	DnaJ protein VC085
8	82	95.3	392	2 S15295	nolC protein - Rhi
9	75	87.2	377	2 R84947	DnaJ protein [impo
10	75	87.2	377	2 JC5609	heat shock protein
11	73	84.9	373	2 D81242	DnaJ protein NMA02
12	73	84.9	375	2 B47042	heat shock protein
13	73	84.9	377	2 D97373	chaperone protein
14	73	84.9	377	2 AD2591	molecular chaperon
15	73	84.9	377	2 AC3502	chaperone protein
16	64	74.4	367	2 I40843	heat shock protein
17	64	74.4	370	2 C71729	DnaJ protein [dnaJ
18	63	73.3	376	2 B70361	chaperone DnaJ - A
19	62	72.1	190	2 B35388	heat shock protein
20	62	72.1	377	2 A83052	DnaJ protein PA476
21	60	69.8	373	2 H87728	DnaJ protein [impo
22	58	67.4	379	2 H86902	DnaJ protein [impo
23	58	67.4	379	2 A47079	heat shock protein
24	58	67.4	385	2 C87250	DnaJ protein [impo
25	57	66.3	352	2 A49210	heat shock protein
26	57	66.3	364	2 D70164	heat shock protein
27	57	66.3	376	2 AD1621	heat shock protein
28	57	66.3	377	2 T43739	heat shock protein
29	57	66.3	377	2 AH1258	heat shock protein

30	56	65.1	368	2 F82570	DnaJ protein XF233
31	56	65.1	372	2 H97528	heat-shock protein
32	56	65.1	378	2 D95060	DnaJ protein [impo
33	53	61.6	499	2 G96831	hypothetical prote
34	52	60.5	372	2 B41874	heat shock protein
35	52	60.5	376	2 H69038	heat shock protein
36	52	60.5	389	2 S41748	heat shock protein
37	50	58.1	297	2 G81329	probable curved-DN
38	50	58.1	348	2 T04618	heat shock protein
39	50	58.1	379	2 B89339	DnaJ protein [impo
40	50	58.1	383	2 E90603	heat shock protein
41	50	58.1	416	2 F71379	heat shock protein
42	49	57.0	335	2 T48161	heat shock protein
43	49	57.0	346	2 B84602	probable DnaJ prot
44	49	57.0	370	2 D83818	heat-shock protein
45	49	57.0	375	2 D82894	heat shock protein

ALIGNMENTS

RESULT 1

HHECDJ

heat shock protein dnaJ - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 30-Jun-1988 #sequence, revision 30-Jun-1988 #text_change 09-Jul-2004

C:Accession: A92572; A26298; S40537; G64721; A26299

R:Bardwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zyllics, M.; Georgopoulos, C.

J. Biol. Chem. 261, 1782-1785, 1986

A:Title: The nucleotide sequence of the Escherichia coli K12 dnaJ gene.

A:Reference number: A92572; MUID:86111850; PMID:3003085

A:Accession: A92572

A:Molecule type: DNA

A:Residues: 1-376 <BAR>

A:Cross-references: UNIPROT:P08622; GB:M12565; NID:g145767; PIDN:AAA23693.1; PID:g145769

A:Experimental source: strain K12

R:Ohki, M.; Tamura, F.; Nishimura, S.; Uchida, H.

J. Biol. Chem. 261, 1778-1781, 1986

A:Title: Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the g

A:Reference number: A26298; MUID:86111849; PMID:3003084

A:Accession: A26298

A:Molecule type: DNA

A:Residues: 1-376 <OHK>

A:Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; GB

R:Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu-

submitted to the EMBL Data Library, December 1992

A:Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2

A:Reference number: S40531

A:Accession: S40537

A:Molecule type: DNA

A:Residues: 1-376 <YUR>

A:Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01292.1; PID:g216441

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G64721

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-376 <BLAT>

A:Cross-references: GB:AE000112; GB:U00096; NID:g1786192; PIDN:AACT3126.1; PID:g1786197;

A:Experimental source: strain K-12, substrain MG1655

C:Comment: This protein is induced by heat shock under the control of the htpR gene prod

C:Genetics:

A:Gene: dnaJ

A:Map position: 0 min

C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C:Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F:5-70/Domain: dnaJ amino-terminal homology <DNJ>

F:77-106/Region: G/F motif

F:144-151/Region: CXXCXGKG repeat

F:161-168/Region: CXXCXGKG repeat

F;183-190/Region: CXXCXGKG repeat
F;197-204/Region: CXXCXGKG repeat

Query Match 100.0%; Score 86; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 2

G90630
DnaJ protein [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)

C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G90630
R;Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.O.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands
A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: G90630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HAY>

A;Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:BA000007; PIDN:BAB33438.1; PID:gl11258796
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:

A;Gene: ECs0015

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 3

G85481
chaperone with DnaK, heat shock protein [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)

C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85481
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G85481

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-376 <STO>

A;Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:AB005174; NID:gl2512693; PIDN:AAQ
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:

A;Gene: dnaJ

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 4

AF0503

DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AF0503

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conner, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AF0503

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-379 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD01166.1; PID:gl6501296; GSPDB:GN00176

C;Genetics:

A;Gene: STY0013

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 5

AB0058
chaperone protein DnaJ [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB0058

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F.;

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AB0058

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-379 <KUR>

A;Cross-references: UNIPROT:Q8ZIM6; GB:AL590842; PIDN:CAC89325.1; PID:gl5978561; GSPDB:G

C;Genetics:

A;Gene: dnaJ

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 6

C64112
heat shock protein dnaJ - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999

C;Accession: C64112

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glöck, A.; Kelley, J.M.; Weidman, J.;

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.;

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, S.;

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: C64112

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-394 <TIGR>

A;Cross-references: GB:L42023; GB:U32803; NID:g1574162; PIDN:AAC22890.1; PID:g1574168; T

C;Genetics:

A;Gene: dnaJ

A;Start codon: GTG

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C;Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F;17-82/Domain: dnaJ amino-terminal homology <DNJ>

F;89-121/Region: G/F motif

F;159-166/Region: CXXCXGXG repeat

F;176-183/Region: CXXCXGXG repeat

F;198-205/Region: CXXCXGXG repeat

F;212-219/Region: CXXCXGXG repeat

Query Match 100.0%; Score 86; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 2.9e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16

|||||:|||||

Db 73 QKRAAYDQYGHAAFEQ 88

RESULT 7

D82270

dnaJ protein VC0856 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: D82270

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952201

A;Accession: D82270

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-381 <HEI>

A;Cross-references: UNIPROT:O34242; GB:AB004171; GB:AB003852; NID:g9655308; PIDN:AAF9401

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0856

A;Map Position: 1

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 96.5%; Score 83; DB 2; Length 381;

Best Local Similarity 93.8%; Pred. No. 9.3e-07;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16

|||||:|||||

Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 8

S15295

nolC protein - Rhizobium fredii

C;Species: Rhizobium fredii

C;Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S15295

R;Krishnan, H.B.; Pueppke, S.G.

Mol. Microbiol. 5, 737-745, 1991

A;Title: nolC, a Rhizobium fredii gene involved in cultivar-specific nodulation of soybe

A;Reference number: S15295; MUID:91260457; PMID:1646377

A;Accession: S15295

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-392 <MOL>

Query Match 87.2%; Score 75; DB 2; Length 377;

Best Local Similarity 86.7%; Pred. No. 2.3e-05;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||:|||||

Db 61 EKRSAYDQYGHAAFE 75

A;Cross-references: UNIPROT:P26508; GB:L03521; NID:g152353; PIDN:AAA26333.1; PID:g152354

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

F;4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 95.1%; Score 82; DB 2; Length 392;

Best Local Similarity 93.8%; Pred. No. 1.4e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16

|||||:|||||

Db 60 QKRAAYDQYGHAAFEQ 75

RESULT 9

F84947

dnaJ protein [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C;Accession: F84947

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: F84947

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-377 <STO>

A;Cross-references: GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: dnaJ; BUI52

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 87.2%; Score 75; DB 2; Length 377;

Best Local Similarity 86.7%; Pred. No. 2.3e-05;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

|||||:|||||

Db 61 EKRSAYDQYGHAAFE 75

RESULT 10

JC5609

heat shock protein dnaJ - Buchnera sp.

C;Species: Buchnera sp.

C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000

C;Accession: JC5609

R;Sato, S.; Ishikawa, H.

J. Biochem. 122, 41-48, 1997

A;Title: Structure and expression of the dnaJ operon of Buchnera, an intracellular symb

A;Reference number: JC5608; MUID:97420684; PMID:9276669

A;Accession: JC5609

A;Molecule type: DNA

A;Residues: 1-377 <SAT>

A;Cross-references: DDBJ:D88673; NID:g2351215; PIDN:BAA21965.1; PID:g2351217

C;Comment: This protein binds to DnaK protein and GrpE protein and modulates the chapero

C;Genetics:

A;Gene: dnaJ

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C;Keywords: DNA replication; heat shock; molecular chaperone

F;5-70/Domain: dnaJ amino-terminal homology <DNJ>

F;77-108/Region: G/F motif

F;145-152/Region: CXXCXGXG repeat

F;162-169/Region: CXXCXGXG repeat

F;184-191/Region: CXXCXGXG repeat

F;198-205/Region: CXXCXGXG repeat

RESULT 15

AC3502
Chaperone protein dnaJ [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3502
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Muejer, C.; Los, T.; Ivanova, N.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Letessier, A.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Letessier, A.; Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <KUR>
A;Cross-references: UNIPROT:Q8YE77; UNIPROT:Q8FXX1; GB:AE008917; PIDN:AAL53182.1; PID:G
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI2001
A;Map position: I
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 84.9%; Score 73; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAFPE 15
Db 60 QKRAAYDRFGHAFPE 74

Search completed: March 7, 2005, 07:42:13
Job time : 10.1722 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 07:21:08 ; Search time 65.5894 Seconds
(without alignments)
124.918 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	86	100.0	372	2 Q7N8Y3	Q7N8Y3 photorhabd
2	86	100.0	375	1 D9AJ_ECOLI	P08622 escherichia
3	86	100.0	376	2 Q7UDU1	Q7UDU1 shigella fl
4	86	100.0	376	2 Q8FLC5	Q8FLC5 escherichia
5	86	100.0	376	2 Q8XA65	Q8XA65 escherichia
6	86	100.0	377	1 D9AJ_HAEDU	P48208 haemophilus
7	86	100.0	378	1 D9AJ_SAUTY	Q60004 salmonella
8	86	100.0	379	2 Q8L3D3	Q8L3D3 colwellia m
9	86	100.0	379	2 Q66ES9	Q66ES9 versinia ps
10	86	100.0	379	2 Q8ZIM6	Q8ZIM6 versinia pe
11	86	100.0	379	2 Q6D088	Q6D088 erwinia car
12	86	100.0	382	1 D9AJ_HAEIN	P43735 haemophilus
13	86	100.0	386	2 Q83ME4	Q83ME4 shigella fl
14	83	96.5	375	1 D9AJ_ACTAC	P77866 actinobacil
15	83	96.5	380	2 Q6LUA6	Q6LUA6 photobacter
16	83	96.5	381	1 D9AJ_VIBCH	Q34242 vibrio chol
17	83	96.5	381	2 Q87R22	Q87R22 vibrio para
18	83	96.5	381	2 Q8DF67	Q8DF67 vibrio vuln
19	83	96.5	385	1 D9AJ_VIBHA	Q87385 vibrio harv
20	83	96.5	386	2 Q7MNS4	Q7MNS4 vibrio vuln
21	83	96.5	389	2 Q65U54	Q65U54 mannheimia
22	82	95.3	379	2 Q92T07	Q92T07 rhizobium m
23	82	95.3	392	1 NOLC_RHIFR	P26508 rhizobium f
24	81	94.2	379	2 Q75WD2	Q75WD2 acetobacter
25	80	93.0	372	1 D9AJ_PASMU	Q9CME2 pasteurella
26	78	90.7	376	2 Q98DD2	Q98DD2 rhizobium l
27	77	89.5	334	1 D9AJ_RHILE	Q33529 rhizobium l
28	77	89.5	231	2 Q93S23	Q93S23 rhizobium t
29	77	89.5	379	1 D9AJ_RHOPA	Q9CNY3 rhodopsu
30	77	89.5	379	1 D9AJ_RHOS7	Q08356 rhodopsu
31	77	89.5	384	2 Q8RB67	Q8RB67 thermocanaer

32	75	87.2	377	1 D9AJ_BUCAI	O32465 buchnera ap
33	75	87.2	377	2 Q7VQL3	Q7VQL3 candidatus
34	75	87.2	379	1 D9AJ_PASHA	O52065 pasteurella
35	75	87.2	383	1 D9AJ_BUCBP	Q89au7 buchnera ap
36	74	86.0	378	1 D9AJ_BUCAP	Q89y9 buchnera ap
37	73	84.9	370	1 D9AJ_ERYRH	Q05646 erysipeloth
38	73	84.9	373	1 D9AJ_NEIMA	P63968 neisseria m
39	73	84.9	373	1 D9AJ_NEIMB	P63969 neisseria m
40	73	84.9	375	1 D9AJ_BROOV	Q05980 brucella ov
41	73	84.9	377	1 D9AJ_AGR5	P50018 agrobacteri
42	73	84.9	377	1 D9AJ_BRAJA	P94319 bradyrhizob
43	73	84.9	377	1 D9AJ_BRUME	Q8ve77 brucella me
44	73	84.9	377	1 D9AJ_BRUSU	Q8fx1 brucella su
45	73	84.9	379	2 Q6RSN5	Q6rsn5 agrobacteri

ALIGNMENTS

RESULT 1

Q7N8Y3 PRELIMINARY; PRT; 372 AA.

AC Q7N8Y3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein dnaJ (HSP40) (Chaperone protein).
GN Name=dnaJ; OrderedLocNames=plu0580;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT01.
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Tacurit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaeser P., Boemare N., Danchin A., Kunst F.,
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
luminescens.";
RT Nat. Biotechnol. 21:1307-1313 (2003).
CC -|- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -|- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; BX571860; CAE12875.1; -.
DR HSSP; P08622; IBOZ.
DR Photolist; plu0580; -.
DR GO; GO:0051082; F:unfolds protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pdp.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJ_PROTEIN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 372 AA; 40820 MW; B2F36918CC6E9B1A CRC64;

Query Match 100.0%; Score 86; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | | | |
Db 61 OKRAAYDQYGHAAFEQ 76

RESULT 2

DNAB ECOLI STANDARD; PRT; 375 AA.
AC P08622;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Chaperone protein dnaJ (Heat shock protein J) (HSP40).
GN Name=dnaJ; Synonyms=groP; OrderedLocusNames=b0015;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RX MEDLINE=86111849; PubMed=3003084;
RA Ohki M., Tamura F., Nishimura S., Uchida H.;
RT "Nucleotide sequence of the Escherichia coli dnaJ gene and
purification of the gene product.";
RL J. Biol. Chem. 261:1778-1781 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=86111850; PubMed=3003085;
RA Bardwell J.C.A., Tilly K., Craig E., King J., Zylicz M.,
RA Georgopoulos C.;
RT "The nucleotide sequence of the Escherichia coli K12 dnaJ+ gene. A
gene that encodes a heat shock protein.";
RL J. Biol. Chem. 261:1782-1785 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92334977; PubMed=1630901;
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
0-2.4 min region.";
RL Nucleic Acids Res. 20:3305-3308 (1992).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [5]
RP POSSIBLE FUNCTION.
RX MEDLINE=91187894; PubMed=1826368;
RA Liberek K., Marszałek J., Ang D., Georgopoulos C., Zylicz M.;
RA "Escherichia coli DnaJ and GrpE heat shock proteins jointly stimulate
ATPase activity of DnaK.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878 (1991).
RN [6]
RP STRUCTURE BY NMR OF 1-107.
RX MEDLINE=96291434; PubMed=8764403; DOI=10.1006/jmbi.1996.0395;
RA Pellechia M., Szyperski T., Wall D., Georgopoulos C., Whetrich K.;
RA "NMR structure of the J-domain and the Gly/Phe-rich region of the
Escherichia coli DnaJ chaperone.";
RL J. Mol. Biol. 260:236-250 (1996).
RN [7]

RP STRUCTURE BY NMR OF 1-104.
RX MEDLINE=99224904; PubMed=10210198;
RA Huang K., Flanagan J.M., Prestegard J.H.;
RT "The influence of C-terminal extension on the structure of the 'J-
domain' in E. coli DnaJ.";
RL Protein Sci. 8:203-214 (1999).
RN [8]
RP STRUCTURE BY NMR OF 130-208.
RX MEDLINE=20351465; PubMed=10891270; DOI=10.1006/jmbi.2000.3923;
RA Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;
RT "Solution structure of the cysteine-rich domain of the Escherichia
coli chaperone protein dnaJ.";
RL J. Mol. Biol. 300:805-818 (2000).
CC -!- FUNCTION: Interacts with dnaK to disassemble a protein complex at
the phase lambda origin of replication. Stimulates, jointly with
grpE, the ATPase activity of dnaK.
CC -!- COFACTOR: Binds 2 zinc ions per monomer.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: By heat shock under the control of the htpR regulatory
protein.
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M12544; AAA00009.1; -;
CC EMBL: M12565; AAA23693.1; -;
CC EMBL: D10483; BAB96590.1; -;
CC EMBL: U00096; AAC73126.1; -;
CC PIR: A92572; HHECDJ.
CC PDB: 1BQ0; NMR; @=1-103.
CC PDB: 1BQ2; NMR; @=1-77.
CC PDB: 1EXK; NMR; A=130-208.
CC PDB: 1XBL; NMR; @=1-107.
CC ECHOBASE; H036.5; 6TH EDITION.
CC EcoGene; EG10240; dnaJ.
CC InterPro: IPR002939; DnaJ C.
CC InterPro: IPR001305; DnaJ_CXXCXGKG.
CC InterPro: IPR001623; DnaJ_N.
CC InterPro: IPR008971; HSP40_dnaJ_pap.
CC InterPro: IPR003095; Hsp DnaJ.
CC InterPro: IPR011031; Multihaem_cyt.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ C; 1.
CC Pfam; PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS; PR00625; DnaJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC PROSITE; PS00636; DnaJ_1; 1.
CC PROSITE; PS00076; DnaJ_2; 1.
CC PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
CC 3D-structure; Chaperone; Complete proteome; Direct protein sequencing;
DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
KW INIT MET 0 0 J-domain.
FT DOMAIN 2 71 Gly-rich.
FT REPEAT 76 113 CXXCXGKG motif.
FT REPEAT 143 150 CXXCXGKG motif.
FT REPEAT 160 167 CXXCXGKG motif.
FT REPEAT 182 189 CXXCXGKG motif.
FT REPEAT 196 203 CXXCXGKG motif.
FT METAL 143 143 Zinc 1.
FT METAL 146 146 Zinc 1.
FT METAL 160 160 Zinc 2.
FT METAL 163 163 Zinc 2.
FT METAL 182 182 Zinc 2.

FT METAL 185 185 Zinc 2.
FT METAL 196 196 Zinc 1.
FT METAL 199 199 Zinc 1.
FT TURN 5 8
FT TURN 9 10
FT TURN 13 14
FT TURN 18 31
FT TURN 32 35
FT TURN 36 38
FT TURN 41 42
FT TURN 43 50
FT TURN 51 51
FT TURN 52 56
FT HELIX 59 64
FT HELIX 65 67
FT TURN 68 73
FT TURN 131 133
FT STRAND 140 142
FT HELIX 144 146
FT TURN 147 149
FT STRAND 151 151
FT STRAND 158 159
FT TURN 161 165
FT STRAND 168 173
FT TURN 174 175
FT STRAND 176 181
FT TURN 183 187
FT STRAND 190 191
FT STRAND 195 195
FT HELIX 197 199
FT TURN 200 201
FT STRAND 204 206
SQ SEQUENCE 375 AA; 40969 MW; 8DE1863CC0BD8C3F CRC64;

Query Match 100.0%; Score 86; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||||
DB 60 QKRAAYDQYGHAAFEQ 75
|||||

RESULT 3

ID Q7UDU1 PRELIMINARY; PRT; 376 AA.
AC Q7UDU1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chapterone with DnaJ; heat shock protein.
GN Name=dnaJ; OrderedLocusNames=S0015;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR HSPB; P08622; IEXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00706; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Heat shock.
SQ SEQUENCE 376 AA; 41072 MW; 1B354AC3F9844532 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||||
DB 61 QKRAAYDQYGHAAFEQ 76
|||||

RESULT 4

Q8FLC5 PRELIMINARY; PRT; 376 AA.
AC Q8FLC5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chapterone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=c0020;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=06:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -I- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -I- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE016755; AAN78520.1; -.
DR PIR; G85481; G85481.
DR PIR; G90630; G90630.
DR HSPB; P08622; IEXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

```
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
DB 61 QKRAAYDQYGHAAFEQ 76

RESULT 5
Q8XA65 PRELIMINARY; PRT; 376 AA.
ID Q8XA65 Q7AHU4;
AC Q8XA65;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chaperone with DnaJ; Heat shock protein (DnaJ protein).
GN Name=dnaJ; OrderedLocustNames=ECs0015, Z0015;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 050952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE005178; AAC54315.1; -.
DR EMBL; AP002550; BAB33438.1; -.
DR FNR; G85481; G85481.
DR FNR; G90630; G90630.
DR HSP; P08622; IEXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.

Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGKG; 1.
PRINTS; PR00625; DnaJPROTEIN.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_2.
PROSITE; PS00636; DnaJ_1; 1.
PROSITE; PS0076; DnaJ_2; 1.
PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc;
KW Complete proteome.
SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
DB 61 QKRAAYDQYGHAAFEQ 76

RESULT 6
DnaJ_HAEU STANDARD; PRT; 377 AA.
ID DnaJ_HAEU
AC P48208;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocustNames=HD0188;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Parsons L.M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; U25996; AAA67299.1; -.
DR EMBL; A5017151; AAP95181.1; -.
DR HSP; P08622; IEXK.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
```

DR Pfam: PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PS00625; DnaJPROTEIN.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 3 72 J-domain.
FT REPEAT 77 108 Gly-rich.
FT REPEAT 147 154 CXXCXGKG motif.
FT REPEAT 164 171 CXXCXGKG motif.
FT REPEAT 186 193 CXXCXGKG motif.
FT REPEAT 200 207 CXXCXGKG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 186 186 Zinc 2 (By similarity).
FT METAL 189 189 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 1 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
SQ SEQUENCE 377 AA; 41027 MW; 37E9048F81A1A7A9 CRC64;
Query Match 100.0%; Score 86; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
RESULT 7
DnaJ_SALTY STANDARD; PRT; 378 AA.
AC Q6004;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chapterone protein dnaJ.
GN Names:dnaJ; OrderedLocusNames:STW0013, STY0013, t0013;
OS Salmonella typhimurium, and
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2;
RA Stephen R.J., Hinton J.C.D.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; Pubmed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Sjaeh J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
[3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; Pubmed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; Pubmed=12844504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Interacts with dnaK to disassemble a protein complex at
the phase lambda origin of replication. Stimulates, jointly with
grpE, the ATPase activity of dnaK.
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By heat shock under the control of the htpR regulatory
protein (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U58360; AAB02911.1; -;
DR EMBL: AB008693; AAL18977.1; -;
DR EMBL: AL627265; CAD01166.1; -;
DR EMBL: AB016834; AAO67747.1; -;
DR HSP; P08622; 1EXX.
DR StyGene; SG10620; dnaJ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_ppe.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 2 71 By similarity.
FT REPEAT 76 112 J-domain.
FT REPEAT 146 153 Gly-rich.
FT REPEAT 163 170 CXXCXGKG motif.
FT REPEAT 185 192 CXXCXGKG motif.
FT REPEAT 199 206 CXXCXGKG motif.
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 149 149 Zinc 1 (By similarity).
FT METAL 163 163 Zinc 2 (By similarity).
FT METAL 166 166 Zinc 2 (By similarity).
FT METAL 185 185 Zinc 2 (By similarity).
FT METAL 188 188 Zinc 2 (By similarity).
FT METAL 199 199 Zinc 1 (By similarity).
FT METAL 202 202 Zinc 1 (By similarity).
SQ SEQUENCE 378 AA; 41181 MW; 176BEC64696F30A2 CRC64;

Query Match 100.0%; Score 86; DB 1; Length 378;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
 DB 60 QKRAAYDQYGHAAFEQ 75

RESULT 8

Q8L3D3 PRELIMINARY; PRT; 379 AA.
 AC Q8L3D3;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Heat shock protein 40.
 GN Name=dnaJ;
 OS Colwellia maris (Vibrio sp. (strain ABF-1)).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Colwelliaceae; Colwellia.
 OX NCBI_TaxID=77524;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Yamauchi S., Okuyama H., Nishiyama Y., Hayashi H.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB084455; BAB91324.2; -
 DR HSP, P08622; 1BQZ.

DR GO; GO:0051082; P:unfolding protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR000345; CytC heme_BS.
 DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.

DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.
 DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.

DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS50076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Heat shock.
 SQ SEQUENCE 379 AA; 40995 MW; 58A2894D13F8E9FA CRC64;

Query Match 100.0%; Score 86; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
 DB 61 QKRAAYDQYGHAAFEQ 76

RESULT 9

Q66ES9 PRELIMINARY; PRT; 379 AA.
 AC Q66ES9;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Heat shock protein, DnaJ and GrpE stimulates ATPase activity of DnaK.
 GN Name=dnaJ; Synonyms=grpC, grpE; ORFNames=YPTB0612;
 OS Yersinia pseudotuberculosis IP 32953.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=273123;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=IP 32953;
 RX PubMed=15358858;
 RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
 RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
 RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser L.J., Garcia E.;
 RT "Insights into the genome evolution of Yersinia pestis through whole
 RT genome comparison with Yersinia pseudotuberculosis";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.

DR EMBL; BX936398; CAH19852.1; -
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR InterPro; IPR002939; DnaJ_C.
 DR InterPro; IPR001305; DnaJ_CXXCXGKG.

DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR008971; HSP40_DnaJ_pap.

DR InterPro; IPR003095; Hsp_DnaJ.
 DR InterPro; IPR011031; Multihem_cyt.

DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS; PR00625; DnaJPROTEIN.

DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS50076; DnaJ_2; 1.

DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.

SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
 DB 61 QKRAAYDQYGHAAFEQ 76

RESULT 10

Q8ZIM6 PRELIMINARY; PRT; 379 AA.
 AC Q8ZIM6; Q74Q12; Q7CG76;
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Chaperone protein DnaJ (Chaperone with DnaK; heat shock protein).
 GN Name=dnaJ; Synonyms=dnaJ2, groP;
 GN OrderedLocusNames=YP3711, YPO469, Y3705;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Farraga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague";
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fothergill J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Niles M.L., Matson J.S., Blattner P.R.,
 RA Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
 RA Han Y., Fang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 DR EMBL: AJ414142; CAB89325.1; -;
 DR EMBL: AE013974; AM87253.1; -;
 DR EMBL: AE017141; AAS63859.1; -;
 DR PIR: AB0058; AB0058.
 DR HSP; P08622; 1EXX.
 DR GO: GO:0051082; F:unfolded protein binding; IEA.
 DR GO: GO:0006457; P:protein folding; IEA.
 DR GO: GO:0006986; P:response to unfolded protein; IEA.
 DR Pfam: PF00226; DnaJ_1.
 DR Pfam: PF01556; DnaJ_C; 1.
 DR Pfam: PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS: PR00625; DnaJPROTEIN.
 DR SMART: SM00271; DnaJ; 1.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN 2.
 DR PROSITE: PS00636; DnaJ_1; 1.
 DR PROSITE: PS50076; DnaJ_2; 1.
 DR PROSITE: PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
 |||||
 Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 11
 Q6D0B8 PRELIMINARY; PRT; 379 AA.
 AC Q6D0B8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Chaperone protein DnaJ.
 GN Name=dnaJ; OrderedLocustNames=ECA3881;
 OS *Erwinia carotovora* (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=29471;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,

RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
 RT "Genome sequence of the enterobacterial phytopathogen *Erwinia*
 RT *carotovora* subsp. atroseptica and characterization of virulence
 RT factors";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
 CC the ATPase activity of dnaK (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the dnaJ family.
 DR EMBL: BX950851; CAG76779.1; -;
 DR GO: GO:0051082; F:unfolded protein binding; IEA.
 DR GO: GO:0006457; P:protein folding; IEA.
 DR InterPro: IPR000345; CytC_heme_BS.
 DR InterPro: IPR002939; DnaJ_C.
 DR InterPro: IPR001305; DnaJ_CXXCXGKG.
 DR InterPro: IPR001623; DnaJ_N.
 DR InterPro: IPR008971; HSP40_DnaJ_pap.
 DR InterPro: IPR003095; Hsp_DnaJ.
 DR InterPro: IPR011031; Multihaem_cyt.
 DR Pfam: PF00226; DnaJ_1.
 DR Pfam: PF01556; DnaJ_C; 1.
 DR Pfam: PF00684; DnaJ_CXXCXGKG; 1.
 DR PRINTS: PR00625; DnaJPROTEIN.
 DR SMART: SM00271; DnaJ; 1.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN 2.
 DR PROSITE: PS00636; DnaJ_1; 1.
 DR PROSITE: PS50076; DnaJ_2; 1.
 DR PROSITE: PS00637; DnaJ_CXXCXGKG; 1.
 KW Chaperone; Complete proteome; DNA replication; Heat shock;
 KW Metal-binding; Repeat; Zinc.
 SQ SEQUENCE 379 AA; 41212 MW; 3814B164D55F8CB9 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
 |||||
 Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 12
 DnaJ_HAEIN STANDARD; PRT; 382 AA.
 ID DnaJ_HAEIN STANDARD; PRT; 382 AA.
 AC P43735;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Chaperone protein DnaJ.
 GN Name=dnaJ; OrderedLocustNames=HI1238;
 OS *Haemophilus influenzae*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; *Haemophilus*.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Karavangelos A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*
 RT Rd.";
 RL Science 269:496-512(1995).

CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U32803; AAC22890.1; ALT_INIT.
CC HSP; P08622; IBOZ.
CC TIGR: H11238;
CC InterPro: IPR002939; DnaJ_C.
CC InterPro: IPR001305; DnaJ_CXXCXGKG.
CC InterPro: IPR001623; DnaJ_N.
CC InterPro: IPR003095; Hsp_DnaJ.
CC InterPro: IPR011031; Multihaem_cyt.
CC Pfam: PF00226; DnaJ_1.
CC Pfam: PF01556; DnaJ_C; 1.
CC Pfam: PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS: PR00625; DnaJPROTEIN.
CC SMART: SM00271; DnaJ; 1.
CC PROSITE: PS00636; DnaJ_1; 1.
CC PROSITE: PS00076; DnaJ_2; 1.
CC PROSITE: PS00637; DnaJ_CXXCXGKG; 1.
CC Chaperone: Complete proteome; DNA replication; Heat shock;
CC Metal-binding; Repeat; Zinc.
CC DOMAIN 3 72 J-domain.
CC DOMAIN 77 110 Gly-rich.
CC REPEAT 147 154 CXXCXGKG motif.
CC REPEAT 164 171 CXXCXGKG motif.
CC REPEAT 186 193 CXXCXGKG motif.
CC REPEAT 200 207 CXXCXGKG motif.
CC METAL 147 147 Zinc 1 (By similarity).
CC METAL 150 150 Zinc 1 (By similarity).
CC METAL 164 164 Zinc 2 (By similarity).
CC METAL 167 167 Zinc 2 (By similarity).
CC METAL 186 186 Zinc 2 (By similarity).
CC METAL 189 189 Zinc 2 (By similarity).
CC METAL 200 200 Zinc 1 (By similarity).
CC METAL 203 203 Zinc 1 (By similarity).
CC SEQUENCE 382 AA; 41222 MW; 8850B88B6FB2BC2B CRC64;
Query Match 100.0%; Score 86; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
RESULT 13
Q83MH4 PRELIMINARY; PRT; 386 AA.
AC Q83MH4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone with DnaK; heat shock protein.
GN Name=dnaJ; OrderedLocNames=SF0015;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Lu W., Wang J., Liu H.,
RA Yang J., Zhang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002). Stimulates, jointly with grpE,
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC EMBL: AE015039; BAA1681.1; -;
CC HSP; P08622; IEKX.
CC GO: GO:0051082; F:DNA replication; IEA.
CC GO: GO:0006260; P:DNA replication; IEA.
CC GO: GO:0006457; P:protein folding; IEA.
CC GO: GO:0006986; P:response to unfolded protein; IEA.
CC InterPro: IPR000345; CytC_heme_BS.
CC InterPro: IPR002939; DnaJ_C.
CC InterPro: IPR001305; DnaJ_N.
CC InterPro: IPR001623; DnaJ_N.
CC InterPro: IPR008971; HSP40 DnaJ_pap.
CC InterPro: IPR003095; Hsp_DnaJ.
CC Pfam: PF00226; DnaJ_1.
CC Pfam: PF01556; DnaJ_C; 1.
CC Pfam: PF00684; DnaJ_CXXCXGKG; 1.
CC PRINTS: PR00625; DnaJPROTEIN.
CC SMART: SM00271; DnaJ; 1.
CC PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_2.
CC PROSITE: PS00636; DnaJ_1; 1.
CC PROSITE: PS00076; DnaJ_2; 1.
CC PROSITE: PS00637; DnaJ_CXXCXGKG; 1.
CC Chaperone: Complete proteome; DNA replication; Heat shock;
CC Metal-binding; Repeat; Zinc.
CC SEQUENCE 386 AA; 42279 MW; 172BC403A6E7D75E CRC64;
Query Match 100.0%; Score 86; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
Db 71 QKRAAYDQYGHAAFEQ 86
RESULT 14
DnaJ_ACTAC STANDARD; PRT; 375 AA.
ID DnaJ_ACTAC
AC P7856;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ;
OS Actinobacillus actinomycetemcomitans (Haemophilus
OS actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y4;
RX MEDLINE=98182595; PubMed=9522128;
RA Yoshida A., Nakano Y., Yamashita Y., Yu H., Ohishi M., Koga T.;
RT "Isolation and characterization of the dnaK operon from
RT Actinobacillus actinomycetemcomitans.";
RL DNA Seq. 8:93-98(1997).
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 CR domain.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D87753; BAA32697.1; -.
DR HSP; P08622; 1BQZ.
DR InterPro; IPR002939; DnaJ C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40 DnaJ_ppep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF02226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
DR Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
KW Chapterone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT DOMAIN 5 70
FT DOMAIN 77 110 Gly-rich.
FT REPEAT 145 152 CXXCXGKG motif.
FT REPEAT 162 169 CXXCXGKG motif.
FT REPEAT 184 191 CXXCXGKG motif.
FT REPEAT 198 205 CXXCXGKG motif.
FT METAL 145 145 Zinc 1 (By similarity).
FT METAL 148 148 Zinc 1 (By similarity).
FT METAL 162 162 Zinc 2 (By similarity).
FT METAL 165 165 Zinc 2 (By similarity).
FT METAL 184 184 Zinc 2 (By similarity).
FT METAL 187 187 Zinc 2 (By similarity).
FT METAL 198 198 Zinc 1 (By similarity).
FT METAL 201 201 Zinc 1 (By similarity).
SQ SEQUENCE 375 AA; 41374 MW; CF9D286756FF44E1 CRC64;

Query Match 96.5%; Score 83; DB 1; Length 375;
Best Local Similarity 93.8%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 EKRAAYDQYGHAAFEQ 76
:|||||
:

RESULT 15
Q6LUAG PRELIMINARY; PRT; 380 AA.
AC Q6LUAG
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative DnaJ protein; DnaJ-class molecular chaperone with C-terminal
DE Zn finger domain.
GN Name=EC0015; OrderedLocusNames=PBPPA0698;
OS Photobacterium profundum (Photobacterium sp. (strain S9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -1- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; CR378665; CAG19119.1; -.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:006457; P:protein folding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40 DnaJ_ppep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF02226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chapterone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 380 AA; 40802 MW; 772DD9F069899B63 CRC64;

Query Match 96.5%; Score 83; DB 2; Length 380;
Best Local Similarity 93.8%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 60 QKRAAYDQYGHAAFEQ 75
:|||||
:

Search completed: March 7, 2005, 07:52:39
Job time : 67.5894 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 07:13:17 ; Search time 77.9868 Seconds
(without alignments)
79.349 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	5 AAU98852	Aau98852 E.coli dn
2	86	100.0	16	6 ABR55126	Adr55126 E. coli d
3	86	100.0	131	3 AAB11396	Aab11396 E. coli e
4	86	100.0	131	4 AAB74197	Aab74197 OmpA-J do
5	86	100.0	131	4 AAB70767	Aab70767 Expressio
6	86	100.0	131	4 AAY72018	Aay72018 E. coli o
7	86	100.0	340	4 AAU17588	Aau17588 Novel sig
8	86	100.0	340	7 ADB94296	Adb94296 Human nov
9	86	100.0	341	7 AAU17587	Aau17587 Novel sig
10	86	100.0	341	7 ADB94295	Adb94295 Human nov
11	86	100.0	373	6 ABM67485	Abm67485 Photorhab
12	86	100.0	376	8 ADR89339	Adr89339 E. coli p
13	86	100.0	376	8 ADN18036	Adn18036 Bacterial
14	86	100.0	378	8 ADN17733	Adn17733 Bacterial
15	86	100.0	378	8 ADS42875	Ads42875 Bacterial
16	86	100.0	380	7 ADF05627	Adf05627 Bacterial
17	86	100.0	380	7 ABO62494	Abo62494 Klebsiell
18	86	100.0	399	3 AAB11395	Aab11395 E. coli e
19	86	100.0	399	4 AAB74196	Aab74196 OmpA-DnaJ
20	86	100.0	399	4 AAB70766	Aab70766 Expressio
21	86	100.0	399	4 RAY72017	Ray72017 E. coli o
22	86	100.0	476	4 ABG17771	Abg17771 Novel hum
23	81	94.2	15	2 AAW25795	Aaw25795 Peptide d
24	81	94.2	15	2 AAY79543	Aay79543 E. coli d
25	81	94.2	15	4 AAM99341	Aam99341 Vaccine r

26	81	94.2	15	5 AAU09842	Aau09842 E.coli dn
27	81	94.2	15	5 AAU98876	Aau98876 E. coli D
28	81	94.2	15	5 AAE19457	Aae19457 Human hea
29	81	94.2	15	6 ABR55132	Adr55132 E. coli D
30	81	94.2	16	4 AAM99344	Aam99344 Vaccine r
31	81	94.2	118	4 AAU02075	Aau02075 Synthetic
32	81	94.2	459	4 AAU02077	Aau02077 Synthetic
33	79	91.9	385	8 ADS21615	Ads21615 Bacterial
34	78	90.7	376	8 ADS23054	Ads23054 Bacterial
35	73	84.9	344	6 ABP80877	Abp80877 N. gonorr
36	72	83.7	15	2 AAR95446	Aar95446 RA suscep
37	72	83.7	15	2 AAW25796	Aaw25796 Peptide d
38	72	83.7	15	5 AAE19458	Aae19458 Heat shoc
39	72	83.7	15	6 ABR55133	Adr55133 E. coli d
40	69	80.2	382	8 ADN25412	Adn25412 Bacterial
41	69	80.2	384	8 ADS43419	Ads43419 Bacterial
42	67	77.9	376	8 ADR31368	Adr31368 Stress re
43	67	77.9	379	8 ADN24677	Adn24677 Bacterial
44	67	77.9	380	8 ADN21920	Adn21920 Bacterial
45	64.5	75.0	14	2 AAR95445	Aar95445 RA suscep

ALIGNMENTS

RESULT 1

AAU98852
ID AAU98852 standard; peptide; 16 AA.

XX AC AAU98852;

XX DT 22-AUG-2002 (first entry)

XX DE E.Coli DnaJ 61 immunogenic peptide.

XX KW Immunogenic peptide; heat shock protein; HSP; DnaJ; immunomodulatory; cytostatic; antiinflammatory; antibacterial; antiarthritic;
XX KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
XX KW infectious disease; inflammatory bowel disease; cancer;
XX KW mucosal tolerisation; DNA vaccination; anergy induction.

XX OS Escherichia coli.

XX PN WO200236611-A2.

XX PD 10-MAY-2002.

XX PF 31-OCT-2001; 2001WO-US045344.

XX PR 01-NOV-2000; 2000US-0245181P.

XX PA (REGC) UNIV CALIFORNIA.

XX PA (MART/) MARTINI A.

XX PI Martini A, Albani S, Carson DA, Prakken BJ;

XX WPI; 2002-489999/52.

XX PT New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory bowel disease or cancer.

XX PS Claim 4; Page 55; 84pp; English.

XX CC This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immune response in a subject. The peptides of the invention may have immunomodulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating (i.e. augmenting/inducing or reducing/inhibiting) an immune response in a subject having an

CC immunological disorder (e.g. autoimmune disease such as arthritis or
CC articular juvenile idiopathic arthritis), an infectious disease, an
CC inflammatory bowel disease or cancer. The immunogenic peptide of the
CC invention is also useful for modulating immunoeffector cell
CC responsiveness in a subject. The immunogenic peptide is particularly
CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
CC general, the peptide is useful in methods involving mucosal tolerisation,
CC DNA vaccination, energy induction or active immunisation. The present
CC sequence represents an E. coli DNAJ immunogenic peptide of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 2
ABR55126
ID ABR55126 standard; peptide; 16 AA.

XX ABR55126;

DT 03-JUL-2003 (first entry)

XX E. coli dnaJ61 antigen-specific epitope peptide.

XX Antigen-specific epitope; immune response; T cell; cytokine;
XX antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
XX cytoskeletal; antithyroid; anti-asthmatic; immunosuppressive;
XX antiparasitic; anti-ulcer; antianaemic; cardiant; respiratory;
XX antiallergic; dermatological; antipsoriatic.

XX Escherichia coli.

XX WO2003026579-A2.

XX 03-APR-2003.

XX 25-SEP-2002; 2002WO-US030578.

XX 25-SEP-2001; 2001US-0325499P.

XX 11-DEC-2001; 2001US-0339284P.

XX (REGC) UNIV CALIFORNIA.

XX Albani S, Martins A;

XX WPI; 2003-430097/40.

XX Modulating an immune response in a subject having an immune-related
XX disorder, e.g. arthritis by administering an antigen-specific epitope and
XX a cytokine or an agent that effects cytokine activity or expression.

XX Disclosure; Page 9; 41pp; English.

XX The invention relates to a novel method for modulating an immune response
XX in a subject having an immune-related disorder. The method comprises: (a)
XX administering an antigen-specific epitope, where administration provides
XX epitope-specific T cell immune modulation; and (b) administering a
XX cytokine, an agent that effects cytokine activity or expression, or an
XX antidiabetic, neuroprotective, anti-inflammatory, cytoskeletal,
XX antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
XX ulcer, antianaemic, cardiant, respiratory general, antiallergic,
XX dermatological, and antipsoriatic activity. The method is useful for
XX modulating an immune response in a subject having an immune-related
XX disorder. The present sequence is used in the exemplification of the

CC invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 3
AAB11396
ID AAB11396 standard; protein; 131 AA.

XX AAB11396;

DT 22-FEB-2001 (first entry)

XX E. coli expression plasmid pUBS520-pIN-J-Domain encoded protein.

XX Eukaryotic protein; protease; interferon; antibody; hormone;
XX disulfide bridge.

XX Escherichia coli.

XX Synthetic.

XX EP1048732-A1.

XX 02-NOV-2000.

XX 26-APR-1999; 99EP-00107412.

XX 26-APR-1999; 99EP-00107412.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX WPI; 2000-674185/66.

XX N-PSDB; AAC66072.

XX Preparation of water-soluble eukaryotic polypeptides with disulfide
XX bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
XX presence of arginine or amide compound.

XX Example 3; Page 17; 40pp; German.

XX This invention describes a novel preparation of a water-soluble,
XX naturally occurring eukaryotic polypeptide containing two or more
XX cysteine units bound via a disulfide bridge which comprises cultivation
XX of prokaryotic cells in the presence of arginine or an amide compound.

XX The method is useful for the preparation of eukaryotic proteins e.g.
XX proteases, interferons, protein hormones, antibodies or antibody
XX fragments (e.g. a single chain FV fragment that binds to thyroid
XX stimulating hormone). It is especially useful for preparing proteins with
XX more than five disulfide bridges, e.g. recombinant plasminogen activator
XX (rPA). The technique is simple and does not require in vitro after-
XX treatment, such as the removal of inclusion bodies, reduction or
XX naturation

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 86; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 84 QKRAAYDQYGHAAFEQ 99

RESULT 4

DR WPI; 2001-033777/05.
 DR N-PSDB; AAD02210.
 XX
 PT Producing water-soluble, naturally folded, and secreted eukaryotic
 PT polypeptide, involves culturing prokaryotic cells containing an
 PT expression vector encoding the polypeptide in the presence of arginine or
 PT a specific compound.
 XX
 XX Example 3; Page 17; 35pp; English.
 PS
 CC The patent discloses a method for the production of a water-soluble,
 CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.
 CC The method involves culturing the prokaryotic cells, containing an
 CC expression vector encoding the desired protein and the prokaryotic signal
 CC sequence, in the presence of an additive, e.g., L-arginine. The signal
 CC sequence mediates the secretion of the desired protein into the
 CC periplasm, where folding of the protein takes place. The prokaryotic cell
 CC also contains an expression vector encoding a molecular chaperone, e.g.,
 CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-
 CC overexpression and co-secretion of molecular chaperones in the periplasm
 CC improves the yield of functionally folded protein. The above method
 CC recombinantly produces a high yield of eukaryotic secreted proteins in
 CC prokaryotes. The method is useful for producing eukaryotic proteins such
 CC as an antibody, antibody fragment, interferon, protein hormone or a
 CC protease. The present sequence is an Escherichia coli outer membrane
 CC protein A (OmpA) signal sequence-J domain fusion protein encoded by
 CC PUBS520-PIN-J-domain. The plasmid, PUBS520-PIN-J-domain, also contains
 CC the lac-Ipp promoter and the Ipp terminator. The periplasmic co-secretion
 CC of J domain, which is the N-terminal portion of the DnaJ, facilitates the
 CC folding of the desired secreted protein
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 86; DB 4; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 OKRAAYDQYGHAAFEQ 16
 Db 84 OKRAAYDQYGHAAFEQ 99
 RESULT 7
 AAU17588
 ID AAU17588 standard; protein; 340 AA.
 XX
 AC AAU17588;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Novel signal transduction pathway protein, Seq ID 1153.
 XX
 KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;
 KW organ transplant rejection; infection; hepatitis C; blood disorder;
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KW reproductive system; gastrointestinal; liver disorder; AIDS;
 KW acquired immune deficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN W0200154733-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001312.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 13-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246534P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
XX XX
(HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
XX N-PSDB; AAS27505.
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
XX prognosing disorders related to the proteins, including cancers, immune
XX disorders and neuronal disorders.
XX

PS Claim 1; SEQ ID NO 1153; 880pp; English.
XX The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX

Query Match 100.0%; Score 86; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
DB 25 QKRAAYDQYGHAAFEQ 40
RESULT 8
ADB94296
ID ADB94296 standard; protein; 340 AA.
XX ADB94296;
XX
DT 04-DEC-2003 (first entry)
XX Human novel protein #530.
XX human; autoimmune disease; Parkinson's disease; silicosis;
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW immunosuppressive agent; adjuvant; enhance immune response;
KW higher affinity antibody induction;
KW increased serum immunoglobulin concentration.
XX
OS Homo sapiens.
XX
PN US2002168711-A1.
XX
PD 14-NOV-2002.
XX
XX 17-JAN-2001; 2001US-00764868.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225467P.
PR 14-AUG-2000; 2000US-0225268P.


```
CC sequences of the invention
XX
    Query Match      100.0%; Score 86; DB 4; Length 341;
    Best Local Similarity 100.0%; Pred. No. 1.3e-06;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QKRAAYDQYGHAAFEQ 16
        |||||
Db      26 QKRAAYDQYGHAAFEQ 41

RESULT 10
ID ADB94295 standard; protein; 341 AA.
XX
AC ADB94295;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human novel protein #529.
XX
KW human; autoimmune disease; Parkinson's disease; silicosis;
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW immunosuppressive agent; adjuvant; enhance immune response;
KW higher affinity antibody induction;
KW increased serum immunoglobulin concentration.
XX
OS Homo sapiens.
XX
XX US2002168711-A1.
XX
PD 14-NOV-2002.
XX
PF 17-JAN-2001; 2001US-00764868.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 23-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
XX WPI: 2003-719985/68.
DR N-PSDB; AD893672.
XX
XX New isolated polypeptide useful for diagnosing and treating
PT immunosuppressive conditions such as autoimmune disease and Parkinson's
PT disease.
XX
XX Claim 11; SEQ ID NO 1152; 345pp; English.
XX
XX The invention relates to an isolated polypeptide. The polypeptide is
CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition in a subject, by determining the presence or
CC amount of expression of the polypeptide in a biological sample and
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition based on the presence or amount of expression of the
CC polypeptide. The polypeptide is also useful for identifying a binding
CC partner to the polypeptide, which involves contacting the polypeptide
CC with a binding partner and determining whether the binding partner
CC effects an activity of the polypeptide. The polypeptide or the nucleic
CC acid encoding the polypeptide is useful for preventing, treating, or
CC ameliorating a medical condition, which involves administering the
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
CC is useful for diagnosing a pathological condition or a susceptibility to
CC a pathological condition in a subject, which involves determining the
CC presence or absence of a mutation in the nucleic acid, and diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC based on the presence or absence of the mutation. The polypeptide, the
CC nucleic acid and an antibody to the polypeptide are useful for treating
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents the amino acid sequence of a novel human
CC protein. Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format direct from
CC USPTO at seqdata.uspto.gov/sequence.html?docID=20020168711.
XX
XX Sequence 341 AA;

Query Match      100.0%; Score 86; DB 7; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QKRAAYDQYGHAAFEQ 16
        |||||
Db      26 QKRAAYDQYGHAAFEQ 41

RESULT 11
AEM67485
ID AEM67485 standard; protein; 373 AA.
XX
```


AC ABM67485;
XX DT 20-NOV-2003 (first entry)
XX DE
XX DE Photorhabdus luminescens protein sequence #582.
XX DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
XX KW detection; food; gene expression; plant; animal; microorganism; toxin;
XX KW antibiotic; biopesticide; virulence factor; disease model; plague;
XX KW whooping cough.
XX OS
XX OS Photorhabdus luminescens.
XX PN WO200294867-A2.
XX PD 28-NOV-2002.
XX PF 07-FEB-2002; 2002WO-IB003040.
XX PF 07-FEB-2001; 2001FR-00001659.
XX PA (INSP) INST PASTEUR.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst P, Danchin A;
XX PI Buchrieser C;
XX DR WPI; 2003-148459/14.
XX XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX PS Claim 2; SEQ ID NO 582; 1205pp; French.
XX CC The invention relates to the isolation of genes and their encoded
XX CC proteins from Photorhabdus luminescens. The isolated sequences are
XX CC sources of probes and primers for detecting the genome of P. luminescens
XX CC and related species; to study polymorphisms; for gene analysis and for
XX CC detection/amplification of the genes. Antibodies (Ab) raised against the
XX CC polypeptides encoded by the genes are used for detection/identification
XX CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
XX CC carry a gene-containing vector are used to select compounds that
XX CC modulate, regulate, induce or inhibit expression of the genes in plants,
XX CC animals or microorganisms other than P. luminescens and are able to alter
XX CC response or sensitivity to toxins and antibiotics produced by P.
XX CC luminescens. Cells transformed to express the genes are useful for
XX CC recombinant production of the proteins, particularly toxins and
XX CC antibacterials useful as insecticides, bactericides and fungicides. The
XX CC genes, proteins, vectors containing the genes and Ab are also useful
XX CC therapeutically (to treat microbial infection by bacteria or fungi that
XX CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
XX CC biopesticides. Other uses of the genes and the proteins are as virulence
XX CC factors and for identifying targets of human diseases for which P.
XX CC luminescens is a model (particularly plague and whooping cough). This
XX CC sequence represents one of the isolated P. luminescens proteins
XX SQ Sequence 373 AA;
Query Match 100.0%; Score 86; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. NO. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
RESULT 12
ADR89339
ID ADR89339 standard; protein; 376 AA.
XX AC ADR89339;
XX XX

DT 18-NOV-2004 (first entry)
XX DE E. coli protein-folding-related factor, DnaJ.
XX DE PPRF; protein-folding-related factor; chaperone; GroES; GroEL; DnaJ;
XX KW DnaJ; GrpE; gene function; cell-free synthesis;
XX KW recombinant protein production; therapeutic protein.
XX OS Escherichia coli.
XX OS WO2004072107-A1.
XX PN 26-AUG-2004.
XX PD 13-FEB-2004; 2004WO-KR000302.
XX PF 15-FEB-2003; 2003KR-00009628.
XX PR (DREA-) DREAMBIOGEN CO LTD.
XX PA Kang SH, Choi WJ, Kim HJ, Jun SY, Lee KY;
XX PI WPI; 2004-616042/59.
XX DR Producing soluble proteins using transformed genes encoding protein-
XX PT folding-related factors in a cell-free protein synthesis system, useful
XX PT in therapeutic, industrial and research purposes.
XX PS Example 1; SEQ ID NO 4; 58pp; English.
XX CC The invention relates to producing soluble protein. The method involves
XX CC preparing cells transformed by genes encoding protein-folding-related
XX CC factors (PPRF), so that the transformed cells can express enhanced levels
XX CC of the PPRF, over-expressing the factors and preparing a cell extract
XX CC for a cell-free protein synthesis system from the transformed cells, and
XX CC producing a high level of soluble protein in the synthesis system
XX CC containing the extract containing the factors. The folding-related factor
XX CC in producing a soluble protein is one or more in number, and/or is a
XX CC chaperone that is GroES/GroEL chaperone family or DnaK/DnaJ/GrpE
XX CC chaperone family. The cell extract is prepared from one or more
XX CC transformed cells. The protein is alpha, beta, gamma-interferon, lipase,
XX CC erythropoietin, cytokines, interleukins, granulocyte-colony stimulating
XX CC factor, granulocyte macrophage-colony stimulating factor, transforming
XX CC growth factors, thrombopoietin, or tissue plasminogen activator. The
XX CC methods and compositions of the present invention are useful for
XX CC producing soluble proteins applicable to therapeutic, industrial and
XX CC research purposes, in particular for assaying functions of newly
XX CC discovered genes. The present sequence represents the amino acid sequence
XX CC of an E. coli DnaJ, a protein-folding-related factor.
XX SQ Sequence 376 AA;
Query Match 100.0%; Score 86; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. NO. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
RESULT 13
ADN18036
ID ADN18036 standard; protein; 376 AA.
XX AC ADN18036;
XX XX 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #689.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX US2003233675-A1.
XX 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 689; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 376 AA;
SQ

Query Match 100.0%; Score 86; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 14
ADN17733
ID ADN17733 standard; protein; 378 AA.
XX
XX AC ADN17733;

XX 02-DEC-2004 (first entry)
DT Bacterial polypeptide #386.
DE
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX US2003233675-A1.
XX 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 386; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 378 AA;
SQ

Query Match 100.0%; Score 86; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 15

AD542875
ID ADS42875 standard; protein; 378 AA.

XX AC ADS42875;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #21305.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

XX PA (HINK/) HINKLE G J.

XX PA (SLAT/) SLATER S C.

XX PA (CHEN/) CHEN X.

XX PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 21305; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 378 AA;

Query Match 100.0%; Score 86; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16
Db 61 OKRAAYDQYGHAAFEQ 76

Search completed: March 7, 2005, 07:40:32
Job time : 79.9868 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 07:42:24 ; Search time 55.6291 Seconds
(without alignments)
94.640 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/RCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	16	14 US-10-001-938-3	Sequence 3, Appli
2	86	100.0	340	9 US-09-764-868-1153	Sequence 1153, Ap
3	86	100.0	341	9 US-09-764-868-1152	Sequence 1152, Ap
4	86	100.0	376	15 US-10-369-493-889	Sequence 689, App
5	86	100.0	378	15 US-10-369-493-386	Sequence 386, App
6	86	100.0	378	15 US-10-369-493-21305	Sequence 21305, A
7	81	94.2	15	9 US-09-756-983-10	Sequence 10, Appl
8	81	94.2	15	9 US-09-828-574-10	Sequence 10, Appl
9	81	94.2	15	14 US-10-001-938-27	Sequence 27, Appl
10	81	94.2	15	14 US-10-299-540-4	Sequence 4, Appli
11	81	94.2	15	14 US-10-299-184-4	Sequence 4, Appli
12	81	94.2	15	14 US-10-239-313A-444	Sequence 444, App
13	81	94.2	16	14 US-10-239-313A-447	Sequence 447, App

14	79	91.9	365	15	US-10-369-493-10648	Sequence 10648, A
15	78	90.7	376	15	US-10-369-493-12087	Sequence 12087, A
16	72	83.7	15	9	US-09-828-574-11	Sequence 11, Appl
17	72	83.7	15	14	US-10-299-540-5	Sequence 5, Appli
18	72	83.7	15	14	US-10-299-184-5	Sequence 5, Appli
19	69	80.2	382	15	US-10-369-493-8065	Sequence 8065, Ap
20	69	80.2	384	15	US-10-369-493-21849	Sequence 21849, A
21	67	77.9	376	16	US-10-375-010-22	Sequence 22, Appl
22	67	77.9	379	15	US-10-369-493-7330	Sequence 7330, Ap
23	67	77.9	380	15	US-10-369-493-4573	Sequence 4573, Ap
24	63	73.3	376	15	US-10-369-493-47	Sequence 47, Appl
25	62	72.1	374	15	US-10-369-493-13658	Sequence 13658, A
26	61	70.9	378	15	US-10-369-493-8450	Sequence 8450, Ap
27	60	69.8	368	9	US-09-861-451A-2	Sequence 2, Appli
28	60	69.8	375	15	US-10-369-493-15859	Sequence 15859, A
29	60	69.8	376	15	US-10-369-493-15487	Sequence 15487, A
30	59	68.6	358	15	US-10-369-493-9641	Sequence 9641, Ap
31	58	67.4	379	15	US-10-369-493-18523	Sequence 18523, A
32	58	67.4	385	15	US-10-369-493-16754	Sequence 16754, A
33	57	66.3	369	15	US-10-369-493-19646	Sequence 19646, A
34	56	65.1	362	15	US-10-369-493-9305	Sequence 9305, Ap
35	56	65.1	378	16	US-10-474-776-634	Sequence 634, App
36	56	65.1	378	17	US-10-472-928-900	Sequence 900, App
37	54	62.8	15	14	US-10-299-540-6	Sequence 6, Appli
38	54	62.8	15	14	US-10-299-184-6	Sequence 6, Appli
39	53	61.6	423	15	US-10-369-493-12619	Sequence 12619, A
40	52	60.5	360	15	US-10-369-493-10371	Sequence 10371, A
41	52	60.5	372	15	US-10-369-493-23206	Sequence 23206, A
42	52	60.5	376	15	US-10-369-493-1212	Sequence 1212, Ap
43	50	58.1	175	16	US-10-767-701-40315	Sequence 40315, A
44	50	58.1	297	15	US-10-282-122A-54551	Sequence 54551, A
45	50	58.1	362	16	US-10-437-963-190831	Sequence 190831,

ALIGNMENTS

RESULT 1
US-10-001-938-3
; Sequence 3, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-3

Query Match 100.0%; Score 86; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 2
US-09-764-868-1153

```
; Sequence 1153, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (110)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (196)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-868-1153

Query Match      100.0%; Score 86; DB 9; Length 340;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
DB 25 QKRAAYDQYGHAAFEQ 40

RESULT 3
US-09-764-868-1152
; Sequence 1152, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1152
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-868-1152

Query Match      100.0%; Score 86; DB 9; Length 341;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
DB 26 QKRAAYDQYGHAAFEQ 41

RESULT 4
US-10-369-493-689
; Sequence 689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 689
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-369-493-689

Query Match      100.0%; Score 86; DB 15; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
DB 61 QKRAAYDQYGHAAFEQ 76

RESULT 5
US-10-369-493-386
; Sequence 386, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 386
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
; US-10-369-493-386

Query Match      100.0%; Score 86; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
DB 61 QKRAAYDQYGHAAFEQ 76

RESULT 6
US-10-369-493-21305
; Sequence 21305, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
```

```
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21305
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-21305

Query Match          100.0%; Score 86; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFEQ 16
   |||||
Db 61 OKRAAYDQYGHAAFEQ 76

RESULT 7
US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJp1 heat shock protein
US-09-756-983-10

Query Match          94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
   |||||
Db 1 OKRAAYDQYGHAAFE 15

RESULT 8
US-09-828-574-10
; Sequence 10, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKSEN, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1
```

```
; CURRENT APPLICATION NUMBER: US/09/828,574
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: dnaJp1 peptide
US-09-828-574-10

Query Match          94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
   |||||
Db 1 OKRAAYDQYGHAAFE 15

RESULT 9
US-10-001-938-27
; Sequence 27, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKSEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Escherichia coli
; OTHER INFORMATION:
US-10-001-938-27

Query Match          94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFE 15
   |||||
Db 1 OKRAAYDQYGHAAFE 15

RESULT 10
US-10-299-540-4
; Sequence 4, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC
; TITLE OF INVENTION: AGAINST ARTHRITIS
; TITLE OF INVENTION: ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
```

; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-540-4

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 11
US-10-299-184-4
; Sequence 4, Application US/10299184
; Publication No. US20030147910A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
; TITLE OF INVENTION: AGAINST ARTHRITIS
; TITLE OF INVENTION: ARTHRITIS
; FILE REFERENCE: UCSD1370-6
; CURRENT APPLICATION NUMBER: US/10/299,184
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-184-4

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 12
US-10-239-313A-444
; Sequence 444, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie

; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-444

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 13
US-10-239-313A-447
; Sequence 447, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 447
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-447

Query Match 94.2%; Score 81; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 14
US-10-369-493-10648
; Sequence 10648, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10648
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Spingomonas aromaticivorans
US-10-369-493-10648

Query Match 91.9%; Score 79; DB 15; Length 365;
Best Local Similarity 87.5%; Pred. No. 3.6e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16
|||||:|||||:
Db 56 OKRAAYDRYGHAAFAQ 71

RESULT 15

US-10-369-493-12087
; Sequence 12087, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12087
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-12087

Query Match 90.7%; Score 78; DB 15; Length 376;
Best Local Similarity 87.5%; Pred. No. 5.5e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16
|||||:|||||:
Db 60 OKRAAYDRYGHAAFEQ 75

Search completed: March 7, 2005, 08:45:18
Job time : 55.6291 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 07:23:03 ; Search time 19.8146 Seconds
(without alignments)
60.278 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AR:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	131	3	US-09-553-498-4
2	86	100.0	131	4	US-09-618-869-4
3	86	100.0	380	4	US-09-543-681A-5912
4	86	100.0	380	4	US-09-489-039A-9011
5	86	100.0	399	3	US-09-553-498-2
6	86	100.0	399	4	US-09-618-869-2
7	81	94.2	15	1	US-08-618-464-4
8	81	94.2	15	3	US-09-107-615-4
9	81	94.2	15	4	US-09-756-983-10
10	81	94.2	15	5	PCT-US95-04896-4
11	72	83.7	15	1	US-08-618-464-5
12	72	83.7	15	3	US-09-107-615-5
13	72	83.7	15	5	PCT-US95-04896-5
14	62	72.1	381	4	US-09-252-991A-27174
15	61	70.9	407	4	US-09-540-236-2899
16	60	69.8	368	4	US-09-861-451A-2
17	56	65.1	352	2	US-08-472-534-6
18	56	65.1	378	4	US-09-583-110-4647
19	56	65.1	379	4	US-09-107-433-3487
20	54	62.8	15	1	US-08-618-464-6
21	54	62.8	15	3	US-09-107-615-6
22	53	61.6	240	4	US-09-248-796A-17703
23	52	60.5	375	4	US-09-328-352-4984
24	47	54.7	138	4	US-09-902-540-13689
25	47	54.7	373	4	US-09-710-279-890
26	47	54.7	385	3	US-09-134-001C-3688
27	46	53.5	419	2	US-08-686-417-3

28 45 52.3 577 4 US-09-252-991A-18102 Sequence 18102, A
29 44 51.2 387 4 US-09-308-992B-11 Sequence 11, Appl
30 44 51.2 397 4 US-09-248-796A-17628 Sequence 17628, A
31 44 51.2 414 4 US-09-308-992B-10 Sequence 10, Appl
32 44 51.2 452 4 US-09-308-992B-29 Sequence 29, Appl
33 44 51.2 453 4 US-09-308-992B-9 Sequence 9, Appl
34 44 51.2 453 4 US-09-308-992B-30 Sequence 30, Appl
35 44 51.2 479 4 US-09-308-992B-28 Sequence 28, Appl
36 44 51.2 480 4 US-09-308-992B-12 Sequence 12, Appl
37 44 51.2 480 4 US-09-252-991A-24992 Sequence 24992, A
38 44 51.2 915 4 US-08-619-554-4 Sequence 4, Appl
39 43 50.0 1895 2 US-09-882-835-4 Sequence 4, Appl
40 41 47.7 87 4 US-09-858-644-4 Sequence 4, Appl
41 41 47.7 223 4 US-09-949-016-6832 Sequence 6832, Ap
42 41 47.7 223 4 US-09-949-016-11497 Sequence 11497, A
43 41 47.7 267 4 US-08-974-546-1 Sequence 1, Appl
44 41 47.7 348 2 US-09-543-681A-7130 Sequence 7130, Ap
45 41 47.7 387 4

ALIGNMENTS

RESULT 1

US-09-553-498-4

; Sequence 4, Application US/09553498

; Patent No. 6309861

; GENERAL INFORMATION:

; APPLICANT: Ambrosius, Dorothee

; APPLICANT: Rudolph, Rainer

; APPLICANT: Schaeffner, Joerg

; APPLICANT: Schwarz, Elisabeth

; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote

; FILE REFERENCE: Case 20379

; CURRENT APPLICATION NUMBER: US/09/553,498

; CURRENT FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: EP99107412.1

; PRIOR FILING DATE: 1999-04-26

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 4

; LENGTH: 131

; TYPE: PRT

; ORGANISM: E. coli

US-09-553-498-4

Query Match 100.0%; Score 86; DB 3; Length 131;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16

Db 84 QKRAAYDQYGHAAFEQ 99

RESULT 2

US-09-618-869-4

; Sequence 4, Application US/09618869

; Patent No. 6455279

; GENERAL INFORMATION:

; APPLICANT: Ambrosius, Dorothee

; APPLICANT: Rudolph, Rainer

; APPLICANT: Schaeffner, Joerg

; APPLICANT: Schwarz, Elisabeth

; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND

; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR

; FILE REFERENCE: 20381

; CURRENT APPLICATION NUMBER: US/09/618,869

; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: EP99114811.5

; PRIOR FILING DATE: 1999-07-29

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: Patentin Ver. 2.1

```

; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-618-869-4

Query Match      100.0%; Score 86; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 84 QKRAAYDQYGHAAFEQ 99

RESULT 3
US-09-543-681A-5912
; Sequence 5912, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5912
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5912

Query Match      100.0%; Score 86; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 63 QKRAAYDQYGHAAFEQ 78

RESULT 4
US-09-489-039A-9011
; Sequence 9011, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9011
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9011

Query Match      100.0%; Score 86; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 64 QKRAAYDQYGHAAFEQ 79

us-10-001-938-3.open.ra1

RESULT 5
US-09-553-498-2
; Sequence 2, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted protei
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 399
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-2

Query Match      100.0%; Score 86; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 84 QKRAAYDQYGHAAFEQ 99

RESULT 6
US-09-618-869-2
; Sequence 2, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-618-869-2

Query Match      100.0%; Score 86; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 84 QKRAAYDQYGHAAFEQ 99

RESULT 7
US-08-618-464-4
; Sequence 4, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
```

```

; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; US-08-618-464-4

Query Match 94.2%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 8
US-09-107-615-4
; Sequence 4, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHROGENIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; US-09-107-615-4

Query Match 94.2%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 9
US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. 6787154
; GENERAL INFORMATION:
; APPLICANT: Albandi, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJp1 heat shock protein
; US-09-756-983-10

Query Match 94.2%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15
```

RESULT 10
PCT-US95-04896-4
; Sequence 4, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US95-04896-4
Query Match 94.2%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
Db 1 OKRAAYDQYGHAAFE 15
RESULT 11
US-08-618-464-5
; Sequence 5, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

STATE: CALIFORNIA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-08-618-464-5
Query Match 83.7%; Score 72; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
Db 2 ERAAYDQYGHAAFE 15
RESULT 12
US-09-107-615-5
; Sequence 5, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

```
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; US-09-107-615-5

Query Match      83.7%; Score 72; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      2 ERAAYDQYGHAAFE 15

; RESULT 14
; US-09-252-991A-27174
; Sequence 27174, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27174
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-27174

Query Match      72.1%; Score 62; DB 4; Length 381;
Best Local Similarity 78.6%; Pred. No. 0.0056;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      66 KRAAYDQYGHAGVD 79

; RESULT 15
; US-09-540-236-2899
; Sequence 2899, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR.
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2899
; LENGTH: 407
; TYPE: PRT
; ORGANISM: M.catarrhalis
; US-09-540-236-2899

Query Match      70.9%; Score 61; DB 4; Length 407;
Best Local Similarity 62.5%; Pred. No. 0.009;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 QKRAAYDQYGHAAFEQ 16
Db      84 EKRAATYDRMGHSAYEQ 99

Search completed: March 7, 2005, 07:55:52
Job time : 20.8146 secs

; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; US-09-107-615-5

Query Match      83.7%; Score 72; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KRAAYDQYGHAAFE 15
Db      2 ERAAYDQYGHAAFE 15

; RESULT 13
; PCT-US95-04896-5
; Sequence 5, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
```

THIS PAGE BLANK (USPIC)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 09:43:27 ; Search time 38 Seconds
(without alignments)
40.512 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2773

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	39.5	11	2 A60656	perisulfakinin - A
2	34	39.5	14	2 A56632	neosulfakinin-II -
3	31	36.0	10	1 GMR012	leucosulfakinin-II
4	31	36.0	10	2 B60656	leucosulfakinin II
5	31	36.0	13	2 S47372	T-cell antigen rec
6	31	36.0	13	2 S47394	T-cell antigen rec
7	30	34.9	11	1 GMR01	leucosulfakinin -
8	30	34.9	13	2 S47368	T-cell antigen rec
9	28	32.6	13	2 S47359	T-cell antigen rec
10	28	32.6	13	2 S47365	T-cell antigen rec
11	28	32.6	13	2 S47374	T-cell antigen rec
12	26	30.2	11	2 PT0214	T-cell receptor be
13	26	30.2	13	2 S47388	T-cell antigen rec
14	26	30.2	13	2 PH1479	T-cell receptor be
15	26	30.2	14	4 152618	hemoglobin beta ch
16	26	30.2	15	2 PH0770	T-cell receptor be
17	25	29.1	13	2 S32471	lymnadFamide 1 - g
18	25	29.1	14	2 PH1586	Ig H chain V-D-J r
19	24	27.9	16	2 PH1622	Ig H chain V-D-J r
20	24	27.9	16	2 PH1589	Ig H chain V-D-J r
21	23	26.7	8	2 S11078	glucose-6-phosphat
22	23	26.7	13	2 S32472	lymnadFamide 2 - g
23	23	26.7	13	2 A60379	factor X activator
24	22	25.6	13	2 S47383	T-cell antigen rec
25	22	25.6	13	2 S32473	lymnadFamide 3 - g
26	22	25.6	15	2 PH1319	Ig heavy chain DJ
27	22	25.6	15	2 P28587	T-cell receptor be
28	22	25.6	15	2 I53284	T-cell receptor be
29	21	24.4	10	2 PT0215	T-cell receptor be

30	21	24.4	12	2 PH0746	T-cell receptor be
31	21	24.4	12	2 PH0771	T-cell receptor be
32	21	24.4	12	2 PH1461	T-cell receptor be
33	21	24.4	13	2 S47361	T-cell antigen rec
34	21	24.4	13	2 I51905	collecting duct wa
35	21	24.4	13	2 S32474	lymnadFamide 4 - g
36	21	24.4	14	2 G44957	photosystem II oxy
37	21	24.4	14	2 PH0755	T-cell receptor be
38	21	24.4	14	2 A17150	glucose 1-dehydrog
39	21	24.4	14	2 S48685	extension protein
40	21	24.4	15	2 PC4269	unidentified OR310
41	20	23.3	10	2 PT0309	Ig heavy chain CRD
42	20	23.3	13	2 G22565	R-phycosythrins ga
43	20	23.3	13	2 PH0168	phosphorylurate hy
44	20	23.3	14	2 PA0013	photosystem II oxy
45	20	23.3	14	2 PT0232	Ig heavy chain CRD

ALIGNMENTS

RESULT 1

A60656

perisulfakinin - American cockroach

C;Species: Periplaneta americana (American cockroach)

C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004

C;Accession: A60656

R;Veenstra, J.A.

Neuropeptides 14, 145-149, 1989

A;Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American

A;Reference number: A60656; PMID:90137190; PMID:2615921

A;Accession: A60656

A;Molecule type: protein

A;Residues: 1-11 <VEE>

A;Cross-references: UNIPROT:P36885

C;Comment: This neuropeptide stimulates hindgut contractions.

C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 39.5%; Score 34; DB 2; Length 11;

Best Local Similarity 55.6%; Pred. No. 8.8;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAAF 14

DB 3 FDDYGHMRP 11

RESULT 2

A56632

neosulfakinin-II - flesh fly (Sarcophaga bullata)

N;Alternate names: Neb-SK-II

N;Contains: neosulfakinin-I (Neb-SK-I)

C;Species: Sarcophaga bullata

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: A56632

R;Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.

Comp. Biochem. Physiol. C 103, 135-142, 1992

A;Title: Isolation and primary structure of two sulfakinin-like peptides from the flesh

A;Reference number: A56632; PMID:93083101; PMID:1360367

A;Accession: A56632

A;Molecule type: protein

A;Residues: 1-14 <FON>

A;Cross-references: UNIPROT:P41493

A;Experimental source: heads

A;Note: Sequence extracted from NCBI backbone (NCBIP:120391)

C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein

F;1-14/Product: neosulfakinin-II #status experimental <NSK2>

F;6-14/Product: neosulfakinin-I #status experimental <NSK1>

F;9/Binding site: sulfate (Tyr) (covalent) #status predicted

F;14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 39.5%; Score 34; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
:|||||
Db 6 FDDYGHMRF 14

RESULT 3
GMROL2
Leucosulfakinin-II - Madeira cockroach
N;Alternate names: LSK-II
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26335
R;Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.
Biochem. Biophys. Res. Commun. 140, 357-364, 1986
A;Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to ch
A;Reference number: A26335; MUID:87048769; PMID:3778455
A;Accession: A26335
A;Molecule type: protein
A;Residues: 1-10 <NAC>
A;Cross-references: UNIPROT:P09039
C;Comment: This peptide was isolated from head extracts. It stimulates muscle contractio
C;Superfamily: Gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Binding site: sulfate (Tyr) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.0%; Score 31; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAAF 14
:|||||
Db 3 DDYGHMRF 10

RESULT 4
B60656
Leucosulfakinin II, non-sulfated - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: B60656
R;Veenstra, J.A.
Neuropeptides 14, 145-149, 1989
A;Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American
A;Reference number: A60656; MUID:90137190; PMID:2615921
A;Accession: B60656
A;Molecule type: protein
A;Residues: 1-10 <VEES>
A;Cross-references: UNIPROT:P09039
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.0%; Score 31; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAAF 14
:|||||
Db 3 DDYGHMRF 10

RESULT 5
S47372
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47372

R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A;Reference number: S47355
A;Accession: S47372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35697; NID:G527485; PIDN:CAA84766.1; PID:G527486
C;Keywords: T-cell receptor

Query Match 36.0%; Score 31; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAAYDOY 9
:|||||
Db 6 RSAYEQY 12

RESULT 6
S47384
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47384
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A;Reference number: S47355
A;Accession: S47384
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35704; NID:G527501; PIDN:CAA84773.1; PID:G527502
C;Keywords: T-cell receptor

Query Match 36.0%; Score 31; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAAYDOY 9
:|||||
Db 6 RSAYEQY 12

RESULT 7
GMROL
Leucosulfakinin - Madeira cockroach
N;Alternate names: LSK
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01622
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch
A;Reference number: A01622; MUID:86315858; PMID:3749893
A;Accession: A01622
A;Molecule type: protein
A;Residues: 1-11 <NAC>
A;Cross-references: UNIPROT:P04428
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.9%; Score 30; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 44;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
:|||||
Db 3 FDDYGHMRF 11

```
RESULT 8
S47368
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47368
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47368
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35693; NID:g527477; PIDN:CAA84762.1; PID:g527478
C;Keywords: T-cell receptor

Query Match      34.9%; Score 30; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RAAYDOY 9
      |||:|
Db      6 RGAYEQY 12

RESULT 9
S47359
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47359
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47359
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35683; NID:g527455; PIDN:CAA84752.1; PID:g527456
C;Keywords: T-cell receptor

Query Match      32.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 RAAYDOY 9
      |||:|
Db      6 RGAYEQY 12

RESULT 10
S47365
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47365; S47375; S47379; S47396; S47397; S47398; S47355
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47365
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35690; NID:g527471; PIDN:CAA84759.1; PID:g527472; EMBL:Z35679;
A;Accession: S47375
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE2>
```

```
A;Cross-references: EMBL:Z35700; NID:g527493; PIDN:CAA84769.1; PID:g527494
A;Accession: S47379
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE3>
A;Cross-references: EMBL:Z35708; NID:g527509; PIDN:CAA84777.1; PID:g527510
A;Accession: S47396
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE4>
A;Cross-references: EMBL:Z35674; NID:g527527; PIDN:CAA84743.1; PID:g527528
A;Accession: S47397
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE5>
A;Cross-references: EMBL:Z35675; NID:g527529; PIDN:CAA84744.1; PID:g527530
A;Accession: S47398
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE6>
A;Cross-references: EMBL:Z35676; NID:g527531; PIDN:CAA84745.1; PID:g527532
C;Keywords: T-cell receptor

Query Match      32.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 RAAYDOY 9
      |||:|
Db      6 RSSYEQY 12

RESULT 11
S47374
T-cell antigen receptor VJ junction beta chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999
C;Accession: S47374; S47399; S47364
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
A;Accession: S47374
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35699; NID:g527491; PIDN:CAA84768.1; PID:g527492; EMBL:Z35689;
A;Accession: S47399
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE2>
A;Cross-references: EMBL:Z35677; NID:g527533; PIDN:CAA84746.1; PID:g527534
C;Keywords: T-cell receptor

Query Match      32.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 RAAYDOY 9
      |||:|
Db      6 RSSYEQY 12

RESULT 12
PT0214
T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0214
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
A;Reference number: PT0209; MUID:91217621; PMID:1902501
```

A;Accession: PT0214
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 30.2%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RAAVDQY 9
| | | | |
Db 4 RGYEQY 10

RESULT 13

S47388
T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47388
R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A;Reference number: S47355

A;Accession: S47388

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: EMBL:Z35710; NID:G527515; PIDN:CAA84779.1; PID:G527516

C;Keywords: T-cell receptor

Query Match 30.2%; Score 26; DB 2; Length 13;

Best Local Similarity 71.4%; Pred. No. 2.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RAAVDQY 9

| | | | |

Db 6 RAAVEQY 12

RESULT 14

PH1479

T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1479

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1479

A;Molecule type: mRNA

A;Residues: 1-13 <CAS>

A;Experimental source: cytolytic T-lymphocyte

C;Keywords: receptor; T-cell

Query Match 30.2%; Score 26; DB 2; Length 13;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RAAVDQY 9

| | | | |

Db 5 QAGYEQY 11

RESULT 15

I52618

hemoglobin beta chain thalassemia mutant Portuguese - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 11-Jul-1996 #text_change 20-Apr-2000

C;Accession: I52618

R;Oner, R.; Oner, C.; Wilson, J.B.; Tamagnini, G.P.; Ribeiro, L.M.; Huisman, T.H.

Br. J. Haematol. 79, 306-310, 1991

A;Title: Dominant beta-thalassaemia trait in a Portuguese family is caused by a deletion

A;Reference number: I52618; MUID:92068764; PMID:1659862

A;Accession: I52618

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-14 <ONE>

A;Cross-references: GB:S68042; NID:G239717; PIDN:AAB20440.1; PID:G239718

C;Genetics:

A;Gene: GDB:HBB

A;Cross-references: GDB:119297; OMIM:141900

A;Map position: 11p15.4-11p15.4

Query Match 30.2%; Score 26; DB 4; Length 14;

Best Local Similarity 50.0%; Pred. No. 2.9e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RAAVDQYGH 12

| | | | |

Db 4 QAAVQKVGRA 13

Search completed: March 7, 2005, 09:58:38

Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 09:10:02 ; Search time 172 Seconds
(without alignments)
47.635 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 7514

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	39.5	9	1 NSK1 SARBU	P41492 sarcophaga
2	34	39.5	11	1 LSKP PERAM	P36885 periplaneta
3	34	39.5	14	1 NSK2 SARBU	P41493 sarcophaga
4	33	38.4	12	1 LOSK LOCW1	P47733 locusta mig
5	31	36.0	10	1 LSK2 LEUMA	P67802 leucophaea
6	31	36.0	10	1 LSK2 PERAM	P67803 periplaneta
7	30	34.9	11	1 LSK1 LEUMA	P04428 leucophaea
8	25	29.1	13	1 NP1 LYMST	P80178 lymnaea sta
9	24	27.9	13	2 Q7S2J9	Q7S2J9 neurospora
10	24	27.9	16	2 O82402	O82402 fragaria nu
11	24	27.9	16	2 O82404	O82404 fragaria ni
12	24	27.9	16	2 O82405	O82405 fragaria ii
13	24	27.9	16	2 O82406	O82406 fragaria mo
14	24	27.9	16	2 O82407	O82407 fragaria vi
15	24	27.9	16	2 O82781	O82781 fragaria ve
16	23	26.7	13	1 NP2 LYMST	P80179 lymnaea sta
17	23	26.7	13	2 Q7LZ24	Q7LZ24 vipera aspi
18	22.5	26.2	16	2 Q5S8A0	Q5S8A0 pinus monti
19	22	25.6	10	2 Q71UL3	Q71UL3 hallotis ru
20	22	25.6	11	2 Q68D59	Q68D59 homo sapien
21	22	25.6	13	1 NP3 LYMST	P80180 lymnaea sta
22	22	25.6	13	2 Q6URV3	Q6URV3 sorghum bic
23	22	25.6	16	2 Q5TNP2	Q5TNP2 homo sapien
24	22	25.6	16	2 Q5S898	Q5S898 lycopersico
25	21	24.4	13	1 NP4 LYMST	P80181 lymnaea sta
26	21	24.4	13	1 P5BP PINPS	P81668 pinus pinas
27	21	24.4	13	2 Q80Y03	Q80Y03 rattus sp.
28	21	24.4	14	2 Q7M0K1	Q7M0K1 streptomyce
29	21	24.4	15	1 ECDA LYMDI	P80938 lymantria d
30	21	24.4	16	2 Q9TRR1	Q9TRR1 oryctolagus
31	20	23.3	9	2 Q93LE4	Q93LE4 heliobacill

32	20	23.3	11	2	O60614	homo sapien
33	20	23.3	11	2	Q9TWM2	Q9TWM2 alysia cal
34	20	23.3	11	2	P89269	P89269 xestia c-ni
35	20	23.3	12	2	O46664	O46664 macropus ro
36	20	23.3	12	2	Q9QVF2	Q9QVF2 rattus sp.
37	20	23.3	13	2	Q7M4Y6	Q7M4Y6 fusarium sp
38	20	23.3	13	2	Q7M268	Q7M268 gastrocioni
39	20	23.3	14	2	Q9FYTO	Q9FYTO allium cepa
40	20	23.3	15	2	Q7M4Z3	Q7M4Z3 fusarium sp
41	20	23.3	15	2	Q9S811	Q9S811 volvox cart
42	20	23.3	15	2	Q9JP39	Q9JP39 pseudomonas
43	20	23.3	15	2	Q7M0G8	Q7M0G8 mus sp. cd3
44	20	23.3	16	2	Q6XA08	Q6XA08 equus cabal
45	20	23.3	16	2	O82403	O82403 fragaria ve

ALIGNMENTS

RESULT 1

NSK1 SARBU STANDARD; PRT; 9 AA.
AC P41492;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neosulfakinin-I (NEB-SK-I).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA MEDLINE=33083101; PubMed=1360367;
RX Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from the fleshfly, Neobellieria bullata.";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -I- FUNCTION: Myotropic peptide.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Sulfation.
FT MOD_RES 4 4 Sulfotyrosine (Potential).
FT MOD_RES 9 9 Phenylalanine amide (Potential).
SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691E8685AAA CRC64;

Query Match 39.5%; Score 34; DB 1; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDQYGHAAF 14
:| ||| |
Db 1 FDDYGHMRF 9

RESULT 2

LSKP PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Perisulfakinin (pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

```

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;
RA Veestra J.A.;
RT "Isolation and structure of two gastrin/CKK-like neuropeptides from
the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -1- FUNCTION: Stimulates hindgut contractions.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656;
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6 6 Sulfotyrosine.
FT MOD_RES 11 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 39.5%; Score 34; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 3 FDDYGHMRF 11

RESULT 3
NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41493;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neosulfakinin-II (NEB-SK-II).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN 1;
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
the fleshfly, Neobellieria bullata.";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: Myotropic peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A56632; A56632.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Sulfation.
FT MOD_RES 9 9 Sulfotyrosine (Potential).
FT MOD_RES 14 14 Phenylalanine amide (Potential).
SQ SEQUENCE 14 AA; 1794 MW; 8B4E06D5B61C62AA CRC64;

Query Match 39.5%; Score 34; DB 1; Length 14;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 6 FDDYGHMRF 14

RESULT 4
LOSK_LOCMI STANDARD; PRT; 12 AA.
AC P47733;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

```

```

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sulfakinin (LOW-SK).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN 1;
RP SEQUENCE.
RC TISSUE=Brain;
RA Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;
RL (in) McCaffery A., Wilson I. (eds.);
RL Chromatography and isolation of insect hormones and pheromones,
pp.231-241, Plenum Press, New York (1990).
CC -1- FUNCTION: Myotropic peptide.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone;
KW Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 7 7 Sulfotyrosine (Potential).
FT MOD_RES 12 12 Phenylalanine amide.
SQ SEQUENCE 12 AA; 1440 MW; 9B5B5DA9BDB5AAA CRC64;

Query Match 38.4%; Score 33; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AYDQYGHAAF 14
Db 3 ASDDYGHMRF 12

RESULT 5
LSK2_LEUMA STANDARD; PRT; 10 AA.
AC P67802; P09039;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leucosulfakinin-II (LSK-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN 1;
RP SEQUENCE.
RX MEDLINE=87048769; PubMed=3778455;
RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
homology to cholecystokinin and gastrin.";
RL Biochem. Biophys. Res. Commun. 140:357-364(1986).
CC -1- FUNCTION: Changes the frequency and amplitude of contractions of
the cockroach hindgut. Stimulates muscle contraction of hindgut.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A26335; GMROL2.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone;
KW Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 5 5 Sulfotyrosine.
FT MOD_RES 10 10 Phenylalanine amide.
SQ SEQUENCE 10 AA; 1255 MW; 9B4F5391E86B5AAA CRC64;

Query Match 36.0%; Score 31; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAAF 14

```

Db 3 DDYGHMRF 10

RESULT 6

LSK2 PERAM

ID LSK2 PERAM STANDARD; PRT; 10 AA.

AC P67803; P09039;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Leucosulfakinin-II (LSK-II).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;

OC Blattidae; Periplaneta.

OC NCBI_TaxID=6978;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;

RA Veenstra J.A.;

RT "Isolation and structure of two gastrin/CKK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.";

RT Neuropeptides 14:145-149(1989).

CC -1- FUNCTION: Changes the frequency and amplitude of contractions of the cockroach hindgut. Stimulates muscle contraction of hindgut.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR PIR; B60656;

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; 1.

KW Amidation; Direct protein sequencing; Hormone;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 Pyrrolidone carboxylic acid.

FT MOD_RES 10 10 Phenylalanine amide.

SQ SEQUENCE 10 AA; 1255 MW; 9B4F5391E86BSAAA CRC64;

Query Match 36.0%; Score 31; DB 1; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DDYGHMRF 14

Db 3 DDYGHMRF 10

RESULT 7

LSK1 LEUMA

ID LSK1 LEUMA STANDARD; PRT; 11 AA.

AC P04428;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Leucosulfakinin-I (LSK-I).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;

OC Blaberidae; Leucophaea.

OC NCBI_TaxID=6988;

RN [1]

RP SEQUENCE.

RX MEDLINE=86315859; PubMed=3749893;

RA Nachman R.J.; Holman G.M.; Haddon W.F.; Ling N.;

RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.";

RL Science 234:71-73(1986).

CC -1- FUNCTION: Changes the frequency and amplitude of contractions of the hindgut. Inhibits muscle contraction of hindgut.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR PIR; A01622; GMR0L.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; 1.

KW Amidation; Direct protein sequencing; Hormone; Sulfation.

FT MOD_RES 6 6 Sulfotyrosine.

FT MOD_RES 11 11 Phenylalanine amide.

SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86BSAAB CRC64;

Query Match 34.9%; Score 30; DB 1; Length 11;

Best Local Similarity 44.4%; Pred. No. 3e+02;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 DDYGHMRF 14

Db 3 DDYGHMRF 11

RESULT 8

NPI LYMST

ID NPI LYMST STANDARD; PRT; 13 AA.

AC P80178;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Lymnaea-DP-amide 1.

OS Lymnaea stagnalis (Great pond snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;

OC Lymnaeidae; Lymnaeidae; Lymnaea.

OC NCBI_TaxID=6523;

RN [1]

RP SEQUENCE.

RC TISSUE=Ganglion;

RX MEDLINE=93238777; PubMed=8477756;

RA Johnsen A.H.; Rehfeld J.F.;

RT "LymnaeaDPamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in invertebrates?";

RT Invertebrates?;

RL Eur. J. Biochem. 213:875-879(1993).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Related to the cholecystokinin (CKK) family.

DR PIR; S32471; S32471.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD_RES 13 13 Phenylalanine amide.

SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 29.1%; Score 25; DB 1; Length 13;

Best Local Similarity 44.4%; Pred. No. 2.6e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 DDYGHMRF 14

Db 2 DDYGHMRF 10

RESULT 9

Q7S2J9

ID Q7S2J9 PRELIMINARY; PRT; 13 AA.

AC Q7S2J9;

DT 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Predicted protein.

GN Name=NCU04977.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OC NCBI_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OR74A;

RA Galagan J.E.; Calvo S.E.; Borkovich K.A.; Selker E.U.; Read N.D.;

RA Jaffe D.; FitzHugh W.; Ma L.-J.; Smirnov S.; Purcell S.; Rehman B.;

RA Elkins T.; Engels R.; Wang S.; Nielsen C.B.; Butler J.; Endrizzi M.;

RA Qui D.; Ianakiev P.; Pedersen D.; Nelson M.; Washburne M.;

RA Selitrennikoff C.P.; Kinsey J.A.; Braun E.L.; Zelter A.; Schulte U.;

RA Kothe G.O.; Jedd G.; Mewes W.; Staben C.; Marcotte B.; Greenberg D.;

RA Roy A.; Foley K.; Naylor J.; Thomann N.; Barrett R.; Gherre S.;

RA Kamal M.; Kamvysselis M.; Maucci E.; Bielek C.; Rudd S.; Frishman D.;

```
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DaSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Flammann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RT Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000422; EAA29651.1; -.
SQ SEQUENCE 13 AA; 1703 MW; 099245360492586B CRC64;

Query Match 27.9%; Score 24; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 AYDQYGHAA 14
| | | |
DB 2 AIDYGYCY 11

RESULT 10
O82402 ID O82402 PRELIMINARY; PRT; 16 AA.
AC O82402;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria nubicola.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=60188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRAS20;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000213; AAC36540.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
| | | |
DB 10 YGHEA 14

RESULT 11
O82404 ID O82404 PRELIMINARY; PRT; 16 AA.
AC O82404;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria nilgerrensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRAS20;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000213; AAC36540.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
| | | |
DB 10 YGHEA 14
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berlin 1;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000217; AAC36544.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
| | | |
DB 10 YGHEA 14

RESULT 12
O82405 ID O82405 PRELIMINARY; PRT; 16 AA.
AC O82405;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria iinumae.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64939;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRAS 377;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000218; AAC36545.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
| | | |
DB 10 YGHEA 14

RESULT 13
O82406 ID O82406 PRELIMINARY; PRT; 16 AA.
AC O82406;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria moschata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRAS 377;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000218; AAC36545.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
| | | |
DB 10 YGHEA 14
```


RP SEQUENCE FROM N.A.
RC STRAIN=FRA 157;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF000219; AAC36546.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR CO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
|||
DB 10 YGHEA 14

RESULT 14

ID 082407 PRELIMINARY; PRT; 16 AA.
AC 082407;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria viridis (Wild strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64942;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 341;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF000220; AAC36547.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR CO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
|||
DB 10 YGHEA 14

RESULT 15

ID 082781 PRELIMINARY; PRT; 16 AA.
AC 082781;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria vesca (Woodland strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=57918;
RN [1]
RP SEQUENCE FROM N.A.

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 09:07:16 ; Search time 159 Seconds
(without alignments)
38.919 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 649094

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp19808:.*
2: Geneseqp19908:.*
3: Geneseqp20008:.*
4: Geneseqp20018:.*
5: Geneseqp20028:.*
6: Geneseqp20038:.*
7: Geneseqp20038s:.*
8: Geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	5	AAU98852 E.Coli DN
2	86	100.0	16	6	ABR55126 E. coli d
3	81	94.2	15	2	AAW25795 Peptide d
4	81	94.2	15	3	AAW79543 E. coli d
5	81	94.2	15	4	AAW99341 Vaccine r
6	81	94.2	15	5	AAU09842 E.coli dn
7	81	94.2	15	5	AAU98876 E.coli D
8	81	94.2	15	5	AAE19457 Human hea
9	81	94.2	15	6	ABR55132 E. coli D
10	81	94.2	16	4	AAW99344 Vaccine r
11	72	83.7	15	2	AAW95446 RA suscep
12	72	83.7	15	2	AAW25796 Peptide d
13	72	83.7	15	5	AAE19458 Heat choc
14	72	83.7	15	6	AAW55133 E. coli d
15	64.5	75.0	14	2	AAW95445 RA suscep
16	54	62.8	15	2	AAW25798 Peptide d
17	54	62.8	15	6	ABR55123 E. coli d
18	34	39.5	9	4	AAU03347 Fruit fly
19	34	39.5	9	4	AAU03346 Fruit fly
20	34	39.5	9	4	AAU03351 Fruit fly
21	34	39.5	9	7	ADEI4680 Drosulfak
22	34	39.5	9	7	ADEI4676 DmGPCR bi
23	34	39.5	9	7	ADEI4679 DmGPCR bi
24	34	39.5	9	7	ADEI4677 DmGPCR bi
25	34	39.5	9	7	ADL83524 Drosophil

26	34	39.5	9	7	ADL83525	Adl83525 Drosophil
27	34	39.5	9	7	ADL83602	Adl83602 Drosophil
28	34	39.5	9	7	ADL83603	Adl83603 Drosophil
29	34	39.5	9	7	ADL83528	Adl83528 Drosophil
30	34	39.5	9	7	ADL83527	Adl83527 Drosophil
31	34	39.5	9	8	ADRO3247	Adr03247 G-protein
32	34	39.5	9	8	ADRO3249	Adr03249 G-protein
33	34	39.5	9	8	ADRO3245	Adr03245 G-protein
34	34	39.5	9	8	ADRO3248	Adr03248 G-protein
35	34	39.5	9	8	ADRO3244	Adr03244 G-protein
36	34	39.5	14	3	AAU03353	AAU03353 Fruit fly
37	34	39.5	14	4	AAU03353	AAU03353 Fruit fly
38	34	39.5	14	6	AAW79793	AAW79793 Peptide 6
39	34	39.5	14	7	ADEI4681	Adel4681 Drosulfak
40	34	39.5	14	7	ADL83529	Adl83529 Drosophil
41	34	39.5	14	8	ADRO3251	Adr03251 Drosophil
42	34	39.5	14	8	ADRO3250	Adr03250 Drosophil
43	34	39.5	15	2	AAU10086	AAU10086 HLA Dw4 i
44	34	39.5	15	2	AAU10089	AAU10089 HLA Dw4p
45	34	39.5	15	2	AAW25799	AAW25799 Synthetic

ALIGNMENTS

RESULT 1
AAU98852
ID AAU98852 standard; peptide; 16 AA.

XX AAU98852;

DT 22-AUG-2002 (first entry)

XX E.Coli DNAJ 61 immunogenic peptide.

KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
KW cytosolic; antiinflammatory; antibacterial; antiarthritic;
KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
KW infectious disease; inflammatory bowel disease; cancer;
KW mucosal toleration; DNA vaccination; anergy induction.

OS Escherichia coli.

XX WO200236611-A2.

XX 10-MAY-2002.

XX 31-OCT-2001; 2001WO-US045344.

XX 01-NOV-2000; 2000US-0245181P.

XX (REGC) UNIV CALIFORNIA.

XX (MART/) MARTINI A.

XX Martini A, Albani S, Carson DA, Prakken BJ;

XX WPI; 2002-489999/52.

XX New immunomodulatory peptides from heat shock proteins, useful for
XX treating immunological disorder in subjects such as humans, e.g.
XX autoimmune disease (e.g. arthritis), infectious disease, inflammatory
XX bowel disease or cancer.

XX Claim 4; Page 55; 84pp; English.

XX This invention relates to the use of a peptide, which is an immunogenic
XX portion derived from a dnaJ heat shock protein (hsp) in modulating an
XX immune response in a subject. The peptides of the invention may have
XX immunomodulatory, cytosolic, antiinflammatory, antibacterial or
XX antiarthritic properties and can stimulate expression of interleukins,
XX tumour necrosis factor and transforming growth factor beta. The
XX immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
XX reducing/inhibiting) an immune response in a subject having an

CC immunological disorder (e.g. autoimmune disease such as arthritis or
 CC articular juvenile idiopathic arthritis), an infectious disease, an
 CC inflammatory bowel disease or cancer. The immunogenic peptide of the
 CC invention is also useful for modulating immunoeffector cell
 CC responsiveness in a subject. The immunogenic peptide is particularly
 CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
 CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
 CC general, the peptide is useful in methods involving mucosal tolerisation,
 CC DNA vaccination, anergy induction or active immunisation. The present
 CC sequence represents an E. coli DNAJ immunogenic peptide of the invention
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKRAAYDQYGHAAFEQ 16
 |||||
 Db 1 OKRAAYDQYGHAAFEQ 16

RESULT 2

ABR55126
 ID ABR55126 standard; peptide; 16 AA.

XX AC ABR55126;

DT 03-JUL-2003 (first entry)

XX E. coli dnaJ61 antigen-specific epitope peptide.

DE Antigen-specific epitope; immune response; T cell; cytokine;
 XX Antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
 KW Cytostatic; antithyroid; anti-asthmatic; immunosuppressive;
 KW Antipsoriatic; anti-ulcer; antianaemic; cardiac; respiratory;
 KW Antiallergic; dermatological; antipsoriatic.

XX Escherichia coli.

XX WO2003026579-A2.

XX 03-APR-2003.

XX 25-SEP-2002; 2002WO-US030578.

XX 25-SEP-2001; 2001US-0325499P.

XX 11-DEC-2001; 2001US-0339284P.

XX (REGC) UNIV CALIFORNIA.

XX Albani S, Martins A;

XX WPI; 2003-430097/40.

XX Modulating an immune response in a subject having an immune-related
 PT disorder, e.g. arthritis by administering an antigen-specific epitope and
 PT a cytokine or an agent that effects cytokine activity or expression.

FS Disclosure; Page 9; 41pp; English.

XX The invention relates to a novel method for modulating an immune response
 CC in a subject having an immune-related disorder. The method comprises: (a)
 CC administering an antigen-specific epitope, where administration provides
 CC epitope-specific T cell immune modulation; and (b) administering a
 CC cytokine, an agent that effects cytokine activity or expression, or an
 CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
 CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
 CC ulcer, antianaemic, cardiac, respiratory general, antiallergic,
 CC dermatological, and antipsoriatic activity. The method is useful for
 CC modulating an immune response in a subject having an immune-related
 CC disorder. The present sequence is used in the exemplification of the

CC invention
 XX Sequence 16 AA;

Query Match 100.0%; Score 86; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKRAAYDQYGHAAFEQ 16
 |||||
 Db 1 OKRAAYDQYGHAAFEQ 16

RESULT 3

AAW25795
 ID AAW25795 standard; peptide; 15 AA.

XX AC AAW25795;

DT 06-APR-1998 (first entry)

DE Peptide dnaJp1 which protects against arthritogenic peptides.

XX dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;
 KW arthritogenic peptide; autoimmune disease; systemic immune system;
 KW anti-dnaJp1 antibody; passive immunisation;
 KW rheumatoid arthritis-susceptibility detection.

XX Escherichia coli.

XX WO9734002-A1.

XX 18-SEP-1997.

XX 20-FEB-1997; 97WO-US002957.

XX 15-MAR-1996; 96US-00618464.

XX (REGC) UNIV CALIFORNIA.

XX Carson DA, Albani S;

XX WPI; 1997-470882/43.

XX Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1
 PT - also determining pre-disposition to rheumatoid arthritis by detecting
 PT anti-arthritogenic peptide antibodies.

PS Disclosure; Page 5; 44pp; English.

XX Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from
 CC Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to induce
 CC relatively strong immune response in seropositive adult rheumatoid
 CC arthritis patients. This peptide was used in a vaccine for protecting
 CC against arthritogenic peptides. The vaccine contains a carrier, pure
 CC dnaJp1 peptide or a recombinant gene expression vector encoding the
 CC dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis (or
 CC other autoimmune diseases). Vaccines can target the arthritogenic
 CC peptides before they are presented to the systemic immune system. Anti-
 CC dnaJp1 antibodies can also be used for passive immunisation. Antibodies
 CC can be used to detect rheumatoid arthritis-susceptibility sequences on
 CC HLA or in populations of E. coli in the gastrointestinal tract

XX Sequence 15 AA;

Query Match 94.2%; Score 81; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKRAAYDQYGHAAFE 15
 |||||
 Db 1 OKRAAYDQYGHAAFE 15

RESULT 4
AA79543
ID AAY79543 standard; peptide; 15 AA.
XX AC
XX AAY79543;
XX DT
XX 15-AUG-2000 (first entry)
XX DE
XX E. coli dnaU1 heat shock protein peptide.
XX KW
XX Antigen presenting cell; T-lymphocyte; T-cell; immunomodulator;
XX KW autoimmune disease; allergy; cancer; infection; graft rejection;
XX KW immunotherapy; therapy; major histocompatibility complex; MHC; dnaU1;
XX KW heat shock protein.
XX OS
XX Escherichia coli.
XX PN
XX WO200023053-A2.
XX PD
XX 27-APR-2000.
XX PF
XX 19-OCT-1999; 99WO-US024666.
XX PR
XX 20-OCT-1998; 98US-0105018P.
XX PA
XX (ALBA/) ALBANI S.
XX PI
XX Albani S;
XX DR
XX WPI; 2000-339492/29.
XX PT
XX New artificial antigen presenting cells useful for isolating and
XX PT expanding T cells, and modulating T cell responses for the treatment of
XX PT e.g. autoimmune diseases, allergies.
XX PS
XX Disclosure; Page 42; 179pp; English.
XX CC
XX This peptide is derived from Escherichia coli heat shock protein dnaU1.
XX CC Novel artificial antigen presenting cells (APC) of the invention comprise
XX CC antigens, such as the present peptide, that are presented by a major
XX CC histocompatibility complex (MHC) component for contact with, and
XX CC recognition by, a T cell receptor. The invention is directed to
XX CC artificial APC and methods of making APC, which are used to isolate and
XX CC expand T cell populations and to modulate T cell responses. The invention
XX CC also provides novel methods for the identification and isolation and
XX CC antigen-specific T cells. The methods provide for the construction of
XX CC liposomes containing MHC:peptide complexes, accessory molecules, co-
XX CC stimulatory molecules, adhesion molecules, and other molecules irrelevant
XX CC to T cell binding or modulation that are used in the binding of
XX CC artificial APC to solid support systems that may be used in the retrieval
XX CC and identification and antigen-specific T cells. Devices and methods are
XX CC provided for treating conditions that would benefit from modulation of T
XX CC cell response, e.g. autoimmune disorders (especially type I diabetes
XX CC mellitus, multiple sclerosis, rheumatoid arthritis, dermatomyositis,
XX CC juvenile rheumatoid arthritis and uveitis), allergies, cancer, viral
XX CC infections, and graft rejection
XX SQ
XX Sequence 15 AA;
Query Match 94.2%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
Db | | | | | | | | | | | | | | | |
1 OKRAAYDQYGHAAFE 15
RESULT 5
AA799341
ID AAM99341 standard; peptide; 15 AA.
XX AC
XX AAM99341;
XX DT
XX 07-DEC-2001 (first entry)
XX DE
XX Vaccine related MHC ligand peptide SEQ ID NO:444.
XX KW
XX Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
XX KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
XX KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
XX KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
XX KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
XX KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
XX KW human immunodeficiency virus.
XX OS
XX Homo sapiens.
XX PN
XX WO200170772-A2.
XX PD
XX 27-SEP-2001.
XX PF
XX 22-MAR-2001; 2001WO-FR000872.
XX PR
XX 23-MAR-2000; 2000FR-00003711.
XX PA
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX PI
XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
XX DR
XX WPI; 2001-611470/70.
XX PT
XX Stabilized pharmaceutical containing N-terminal glutamic acid or
XX PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
XX PT with strong acid.
XX PS
XX Claim 9; Page 107; 149pp; French.
XX CC
XX The present invention describes a pharmaceutical compound (I) that
XX CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
XX CC the form of an addition salt with a strong, physiologically acceptable
XX CC acid (II). Also described are: (a) a pharmaceutical composition
XX CC containing at least one (I); (b) a vaccine containing at least one (I)
XX CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
XX CC method for in vitro diagnosis of diseases associated with the presence of
XX CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
XX CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
XX CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
XX CC cytostatic activities. (I) are useful in human or veterinary medicine,
XX CC in pharmaceutical compositions (for treating immune disorders, e.g.
XX CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
XX CC rejection, infection, hormonal disorders and central nervous system
XX CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
XX CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
XX CC infections; or (ii) of cancers. A particular application is in anti-
XX CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
XX CC associated with interactions between MHC and (I), e.g. melanoma and human
XX CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
XX CC which can be used in pharmaceutical compounds from the present invention
XX SQ
XX Sequence 15 AA;
Query Match 94.2%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
Db | | | | | | | | | | | | | | | |
1 OKRAAYDQYGHAAFE 15
RESULT 6
AAU09842
ID AAU09842 standard; peptide; 15 AA.
XX AC
XX AAU09842;
XX DT
XX 07-DEC-2001 (first entry)
XX DE
XX Vaccine related MHC ligand peptide SEQ ID NO:444.
XX KW
XX Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
XX KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
XX KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
XX KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
XX KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
XX KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
XX KW human immunodeficiency virus.
XX OS
XX Homo sapiens.
XX PN
XX WO200170772-A2.
XX PD
XX 27-SEP-2001.
XX PF
XX 22-MAR-2001; 2001WO-FR000872.
XX PR
XX 23-MAR-2000; 2000FR-00003711.
XX PA
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX PI
XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
XX DR
XX WPI; 2001-611470/70.
XX PT
XX Stabilized pharmaceutical containing N-terminal glutamic acid or
XX PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
XX PT with strong acid.
XX PS
XX Claim 9; Page 107; 149pp; French.
XX CC
XX The present invention describes a pharmaceutical compound (I) that
XX CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
XX CC the form of an addition salt with a strong, physiologically acceptable
XX CC acid (II). Also described are: (a) a pharmaceutical composition
XX CC containing at least one (I); (b) a vaccine containing at least one (I)
XX CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
XX CC method for in vitro diagnosis of diseases associated with the presence of
XX CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
XX CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
XX CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
XX CC cytostatic activities. (I) are useful in human or veterinary medicine,
XX CC in pharmaceutical compositions (for treating immune disorders, e.g.
XX CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
XX CC rejection, infection, hormonal disorders and central nervous system
XX CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
XX CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
XX CC infections; or (ii) of cancers. A particular application is in anti-
XX CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
XX CC associated with interactions between MHC and (I), e.g. melanoma and human
XX CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
XX CC which can be used in pharmaceutical compounds from the present invention
XX SQ
XX Sequence 15 AA;
Query Match 94.2%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OKRAAYDQYGHAAFE 15
Db | | | | | | | | | | | | | | | |
1 OKRAAYDQYGHAAFE 15

```
AC AAU09842;
XX
XX
XX 26-FEB-2002 (first entry)
XX
XX E.coli dnaJp1 heat shock protein-derived peptide.
XX
XX Antigenic; antidiabetic; neuroprotective; antirheumatic; antiarthritic;
XX dermatological; immunosuppressive; ophthalmological; antiallergic;
XX cytotatic; virucide; antibacterial; artificial antigen presenting cell;
XX liposome; major histocompatibility complex; MHC; T cell; allograft;
XX cytokine production; T-helper 2 response; transplantation therapy;
XX autoimmune disease; type I diabetes mellitus; multiple sclerosis;
XX rheumatoid arthritis; dermatomyositis; juvenile rheumatoid arthritis;
XX uveitis; allergy; cancer; infection; dnaJp1 heat shock protein.
XX
XX Escherichia coli.
XX
XX WO200180833-A1.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2000; 2000WO-IT000161.
XX
XX 20-APR-2000; 2000WO-IT000161.
XX
XX (ALBA/) ALBANI S.
XX
XX Albani S;
XX
XX WPI; 2002-055316/07.
XX
XX New artificial antigen presenting cell, useful for modulating T cell
XX response for treating allergies and cancers, comprises liposome, major
XX histocompatibility complex, antigen and accessory molecule components.
XX
XX Disclosure; Page 46; 195pp; English.
XX
XX The invention relates to an artificial antigen presenting cell (1)
XX comprising liposome, major histocompatibility complex (MHC), antigen and
XX accessory molecule components. (1) is used in methods for the following:
XX (1) identifying T cells specific for an antigen of interest; (2)
XX isolating T cells specific for an antigen of interest; (3) modulating T
XX cell response; (4) characterising the functional state of antigen-
XX specific T cells; (5) treating a condition in a subject which would be
XX benefited by altering the functional pattern of cytokine production by
XX certain antigen-specific T cells to increase T-helper (Th) 2 response
XX and/or decrease Th1 response; (6) identifying antigen-specific T cells
XX specific for epitopes on a graft donor's tissue likely to elicit graft
XX versus host rejection response; and (7) treating a recipient mammal to
XX reduce rejection of allografts in a transplantation therapy regime.
XX Method (5) is useful for treating autoimmune disease such as type I
XX diabetes mellitus, multiple sclerosis, rheumatoid arthritis,
XX dermatomyositis, juvenile rheumatoid arthritis or uveitis. Alternatively
XX it is useful for treating allergy due to allergens such as dust, animal
XX skin bypass products, vegetables, fruits, pollen or chemicals, cancer,
XX viral infection, bacterial infection. Addition of the accessory
XX molecules, as well as co-stimulatory molecules, and other proteins in
XX proper orientation in the liposomes allow for substantially improved
XX binding association and manipulation of T cells which is very important
XX in the identification and stimulation of antigen-specific T cells. The
XX present sequence represents E.coli dnaJp1 heat shock protein-derived
XX peptide used in the method of the invention
XX
XX Sequence 15 AA;
XX
XX Query Match 94.2%; Score 81; DB 5; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 OKRAAYDOYGHAAFE 15
XX |||||
XX Db 1 OKRAAYDOYGHAAFE 15
XX |||||
XX
XX RESULT 8
XX
XX RESULT 7
XX
XX AAU98876
XX
XX ID AAU98876 standard; peptide; 15 AA.
XX
XX AC AAU98876;
XX
XX 22-AUG-2002 (first entry)
XX
XX E. coli DNAJ PI immunogenic peptide.
XX
XX Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
XX cytotatic; antiinflammatory; antibacterial; antiarthritic; human;
XX autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
XX infectious disease; inflammatory bowel disease; cancer; HDJ2;
XX mucosal tolerisation; DNA vaccination; anergy induction.
XX
XX Escherichia coli.
XX
XX WO200236611-A2.
XX
XX 10-MAY-2002.
XX
XX 31-OCT-2001; 2001WO-US045344.
XX
XX 01-NOV-2000; 2000US-0245181P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (MART/) MARTINI A.
XX
XX Martini A, Albani S, Carson DA, Prakken BJ;
XX WPI; 2002-489999/52.
XX
XX New immunomodulatory peptides from heat shock proteins, useful for
XX treating immunological disorder in subjects such as humans, e.g.
XX autoimmune disease (e.g. arthritis), infectious disease, inflammatory
XX bowel disease or cancer.
XX
XX Example 8; Page 53; 84pp; English.
XX
XX This invention relates to the use of a peptide, which is an immunogenic
XX portion derived from a dnaJ heat shock protein (hsp) in modulating an
XX immune response in a subject. The peptides of the invention may have
XX immunomodulatory, cytostatic, antiinflammatory, antibacterial or
XX antiarthritic properties and can stimulate expression of interleukins,
XX tumour necrosis factor and transforming growth factor beta. The
XX immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
XX reducing/inhibiting) an immune response in a subject having an
XX immunological disorder (e.g. autoimmune disease such as arthritis or
XX articular juvenile idiopathic arthritis), an infectious disease, an
XX inflammatory bowel disease or cancer. The immunogenic peptide of the
XX invention is also useful for modulating immunoeffector cell
XX responsiveness in a subject. The immunogenic peptide is particularly
XX useful for treating the above-mentioned diseases in mammals, e.g. cat,
XX dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
XX general, the peptide is useful in methods involving mucosal tolerisation,
XX DNA vaccination, anergy induction or active immunisation. The present
XX sequence represents the E.coli DNAJ PI immunogenic peptide of the
XX invention
XX
XX Sequence 15 AA;
XX
XX Query Match 94.2%; Score 81; DB 5; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 OKRAAYDOYGHAAFE 15
XX |||||
XX Db 1 OKRAAYDOYGHAAFE 15
XX |||||
```

```
AAE19457
ID AAE19457 standard; peptide; 15 AA.
XX
AC AAE19457;
XX
XX
DT 31-MAY-2002 (first entry)
XX
DE Human heat shock protein (hsp) dnaJp1 peptide.
XX
XX Human; human leukocyte antigen; HLA; DR-binding peptide; therapy;
KW stress protein; major histocompatibility complex; MHC; antiulcer;
KW type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;
KW rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;
KW ulcerative colitis; infectious disease; haemostatic; nephrotropic;
KW polymyositis; chronic active hepatitis; primary biliary cirrhosis;
KW pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;
KW Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;
KW inflammatory bowel disease; Goodpasture's syndrome; neuroprotective;
KW antimicrobial; immunosuppressive; dermatological; antiinflammatory;
KW antiinfertility; idiopathic Addison's disease; cytostatic.
XX
OS Homo sapiens.
XX
XX WO200212286-A2.
XX
XX 14-FEB-2002.
XX
XX 08-AUG-2001; 2001WO-US041656.
XX
XX 09-AUG-2000; 2000US-0224104P.
XX
XX 06-APR-2001; 2001US-00828574.
XX
XX (UYCA-) UNIV CALIFORNIA SAN DIEGO.
XX
XX Albani S, Prakken BJ;
XX
XX WPI; 2002-227137/28.
XX
XX Novel human leukocyte antigen pan DR-binding peptide, useful for treating
XX immune mediated diseases and conditions, has a fragment of stress protein
XX that binds to major histocompatibility complex class II molecules.
XX
XX Claim 9; Page 45; 68pp; English.
XX
XX The invention relates to human leukocyte antigen (HLA) pan DR-binding
XX peptide comprising a fragment of a stress protein that binds to one or
XX more major histocompatibility complex (MHC) class II molecules. The
XX invention also relates to heat shock protein (hsp) peptides. The peptides
XX of the invention and the immunomodulating composition comprising these
XX peptides are useful for modulating, treating or preventing an immune-
XX mediated disease in a mammalian subject e.g. human, having or at risk of
XX having a disease including autoimmune disease, multiple sclerosis (MS),
XX rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I
XX diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,
XX lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,
XX retinoblastoma, sarcoma and connective tissue cancers) and infectious
XX diseases. The peptides of the invention are also useful for screening
XX peptides or analogues that modulate pathogenic immune response. These
XX peptides are useful for treating autoimmune diseases or disorders
XX including Sjogren's syndrome, polymyositis, chronic active hepatitis,
XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease,
XX gluten-sensitive enteropathy, Grave's disease, inflammatory bowel
XX disease, autoimmune neuropathia, idiopathic thrombocytopenia purpura,
XX pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,
XX bullous pemphigoid, discoid lupus and dense deposit disease. The present
XX sequence is human hsp dnaJp1 peptide used in the exemplification of the
XX invention
XX
XX Sequence 15 AA;
XX
XX Query Match 94.2%; Score 81; DB 5; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-07;
XX
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QKRAAYDQYGHAAFE 15
XX |||||
XX Db 1 QKRAAYDQYGHAAFE 15
XX |||||
XX
XX RESULT 9
XX ABR55132
XX ID ABR55132 standard; peptide; 15 AA.
XX
XX AC ABR55132;
XX
XX 03-JUL-2003 (first entry)
XX
XX E. coli DnaJp1 antigen-specific epitope peptide.
XX
XX Antigen-specific epitope; immune response; T cell; cytokine;
XX antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
XX cytotatic; antithyroid; anti-asthmatic; immunosuppressive;
XX antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
XX antiallergic; dermatological; antipsoriatic.
XX
XX Escherichia coli.
XX
XX WO2003026579-A2.
XX
XX 03-APR-2003.
XX
XX 25-SEP-2002; 2002WO-US030578.
XX
XX 25-SEP-2001; 2001US-0325499P.
XX
XX 11-DEC-2001; 2001US-0339284P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Albani S, Martins A;
XX
XX WPI; 2003-430097/40.
XX
XX Modulating an immune response in a subject having an immune-related
XX disorder, e.g. arthritis by administering an antigen-specific epitope and
XX a cytokine or an agent that effects cytokine activity or expression.
XX
XX Disclosure; Page 9; 41pp; English.
XX
XX The invention relates to a novel method for modulating an immune response
XX in a subject having an immune-related disorder. The method comprises: (a)
XX administering an antigen-specific epitope, where administration provides
XX epitope-specific T cell immune modulation; and (b) administering a
XX cytokine, an agent that effects cytokine activity or expression, or an
XX anticytokine therapy. The method of the invention has antiarthritic,
XX antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
XX antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
XX ulcer, antianaemic, cardiant, respiratory general, antiallergic,
XX dermatological, and antipsoriatic activity. The method is useful for
XX modulating an immune response in a subject having an immune-related
XX disorder. The present sequence is used in the exemplification of the
XX invention
XX
XX Sequence 15 AA;
XX
XX Query Match 94.2%; Score 81; DB 6; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-07;
XX
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QKRAAYDQYGHAAFE 15
XX |||||
XX Db 1 QKRAAYDQYGHAAFE 15
XX |||||
XX
XX RESULT 10
XX AAM99344
```

AA099344 standard; peptide; 16 AA.
AA099344;
07-DEC-2001 (first entry)
Vaccine related MHC ligand peptide SEQ ID NO:447.
Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC; immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virus.
Homo sapiens.
W0200170772-A2.
27-SEP-2001.
22-MAR-2001; 2001WO-FR000872.
23-MAR-2000; 2000FR-00003711.
(FABR) FABRE MEDICAMENT SA PIERRE.
Klinguer-Hamouir C, Corvaia N, Beck A, Goetsch L;
WPI; 2001-611470/70.
Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt with strong acid.
Claim 9; Page 107; 149pp; French.
The present invention describes a pharmaceutical compound (I) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a vaccine containing at least one (I) containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomodulator, endocrine, antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders, e.g. immune deficiency, autoimmune states, hypersensitivity, allergy, graft rejection, infection, hormonal disorders and central nervous system diseases), also, where (I) is a MHC ligand (Ia), in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections; or (ii) of cancers. A particular application is in anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection. AA099898 to AA099592 represent peptides which can be used in pharmaceutical compounds from the present invention

SQ Sequence 16 AA;

Query Match 94.2%; Score 81; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | |
Db 1 OKRAAYDQYGHAAFE 15

RESULT 11
AA095446

AA095446 standard; peptide; 15 AA.
AA095446;
01-JUL-1996 (first entry)
RA susceptibility sequence peptide #2.
Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody; arthritogenic peptide; RA-beggn bacteria; Escherichia; Lactococcus; Klebsiella; Proteus; therapy.
Synthetic.
Key Location/Qualifiers
Region 1..5
FT Misc-difference 1 /note= "rheumatoid arthritis susceptibility sequence"
FT Misc-difference 2 /note= "Q1D"
FT Misc-difference 2 /note= "K2E"
W09531984-A1.
30-NOV-1995.
24-APR-1995; 95WO-US004896.
20-MAY-1994; 94US-00246988.
(REGC) UNIV CALIFORNIA.
Carson DA, Salvatore A;
WPI; 1996-020344/02.
Treatment of rheumatoid arthritis - by limiting exposure of immune system to arthritogenic peptide(s).
Example 3; Page 36; 52pp; English.
AA095445 and AA095446 represent rheumatoid arthritis (RA) susceptibility sequence (see AA095443 and AA095444) containing peptides. This sequence corresponds to a region of dnaJ. These sequences are present on arthritogenic proteins and are targeted in this invention as antibody recognition sites. The anti-arthritogenic peptide antibodies that are developed can then be administered to a patient who has RA or who is predisposed to develop RA, to reduce the exposure to arthritogenic peptides. The antibodies are produced and administered in milk. An alternative treatment method comprises the administration of a non-adsorbable antibiotic, together with a RA-beggn bacteria (selected from the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the patient who has RA (or a predisposition to it). Candidates for either of these methods can be screened by detecting an in-vitro cellular immune response to an arthritogenic peptide. The method of the invention allows for the reduction of sensitization to microbial arthritogenic peptides (such as dnaJ). It also limits the exposure of the systemic immune system of humans to RA arthritogenic peptides present in the gastrointestinal tract
SQ Sequence 15 AA;

Query Match 83.7%; Score 72; DB 2; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
: | | | | | | | | | | | | | |
Db 2 ERAAYDQYGHAAFE 15

RESULT 12
AAW25796

AAW25796 standard; peptide; 15 AA.
AAW25796;
06-APR-1998 (first entry)
Peptide dnaJpV which protects against arthritogenic peptides.
dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;
arthritogenic peptide; autoimmune disease; systemic immune system;
anti-dnaJp1 antibody; passive immunisation;
rheumatoid arthritis-susceptibility detection.
Synthetic.
Escherichia coli.
Key Location/Qualifiers
Misc-difference 1 /label= Q1D
FT /note= "wild type Gln substituted with Asp"
FT Misc-difference 2 /label= K2E
FT /note= "wild type Lys substituted with Glu"
W09734002-A1.
18-SEP-1997.
20-FEB-1997; 97WO-US002957.
15-MAR-1996; 96US-00618464.
(REGC) UNIV CALIFORNIA.
Carson DA, Albani S;
WPI; 1997-470882/43.
Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1
- also determining pre-disposition to rheumatoid arthritis by detecting
anti-arthritogenic peptide antibodies.
Disclosure; Page 5; 44pp; English.
Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from
Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to induce
relatively strong immune response in seropositive adult rheumatoid
arthritis patients. This peptide was used in a vaccine for protecting
against arthritogenic peptides. The vaccine contains a carrier, pure
dnaJp1 peptide or a recombinant gene expression vector encoding the
dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis (or
other autoimmune diseases). Vaccines can target the arthritogenic
peptides before they are presented to the systemic immune system. Anti-
dnaJp1 antibodies can also be used for passive immunisation. Antibodies
can be used to detect rheumatoid arthritis-susceptibility sequences on
HLA or in populations of E. coli in the gastrointestinal tract
Sequence 15 AA;
Query Match 83.7%; Score 72; DB 2; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15
:|||||
RESULT 13
AAE19458
ID AAE19458 standard; peptide; 15 AA.
XX AAE19458;
AC

31-MAY-2002 (first entry)
Heat shock protein (hsp) dnaJpV peptide.
Human leukocyte antigen; HLA; DR-binding peptide; therapy;
stress protein; major histocompatibility complex; MHC; antiulcer;
type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;
rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;
ulcerative colitis; infectious disease; haemostatic; nephrotropic;
polymyositis; chronic active hepatitis; primary biliary cirrhosis;
pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;
Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;
inflammatory bowel disease; Goodpasture's syndrome; neuroprotective;
antimicrobial; immunosuppressive; dermatological; antiinflammatory;
antiinfertility; idiopathic Addison's disease; cytostatic.
Unidentified.
W0200212286-A2.
14-FEB-2002.
08-AUG-2001; 2001WO-US041656.
09-AUG-2000; 2000US-0224104P.
06-APR-2001; 2001US-00828574.
(UYCA-) UNIV CALIFORNIA SAN DIEGO.
Albani S, Prakken BJ;
WPI; 2002-227137/28.
Novel human leukocyte antigen pan DR-binding peptide, useful for treating
immune mediated diseases and conditions, has a fragment of stress protein
that binds to major histocompatibility complex class II molecules.
Example 3; Page 46; 68pp; English.
The invention relates to human leukocyte antigen (HLA) pan DR-binding
peptide comprising a fragment of a stress protein that binds to one or
more major histocompatibility complex (MHC) class II molecules. The
invention also relates to heat shock protein (hsp) peptides. The peptides
of the invention and the immunomodulating composition comprising these
peptides are useful for modulating, treating or preventing an immune-
mediated disease in a mammalian subject e.g. human, having or at risk of
having a disease including autoimmune disease, multiple sclerosis (MS),
rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I
diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,
lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,
retinoblastoma, sarcoma and connective tissue cancers) and infectious
diseases. The peptides of the invention are also useful for screening
peptides or analogues that modulate pathogenic immune response. These
peptides are useful for treating autoimmune diseases or disorders
including Sjogren's syndrome, polymyositis, chronic active hepatitis,
mixed connective tissue disease, primary biliary cirrhosis, pernicious
anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease,
gluten-sensitive enteropathy, Grave's disease, inflammatory bowel
disease, autoimmune neutropenia, idiopathic thrombocytopenia purpura,
pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,
bullous pemphigoid, discoid lupus and dense deposit disease. The present
sequence is hsp dnaJpV peptide used in the exemplification of the
invention
Sequence 15 AA;
Query Match 83.7%; Score 72; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
:|||||
SQ

01-JUL-1996 (first entry)

RA susceptibility sequence peptide #1.

Rheumatoid arthritis; RA; dnaJ; E. coli; heat shock protein; antibody; arthritogenic peptide; RA-beggn bacteria; Escherichia; Lactococcus; Klebsiella; Proteus; therapy.

Escherichia coli.

Key Location/Qualifiers
Region 1..5
/note= "rheumatoid arthritis susceptibility sequence"

WO95311984-A1.

30-NOV-1995.

24-APR-1995; 95WO-US004896.

20-MAY-1994; 94US-00246988.

(REGC) UNIV CALIFORNIA.

Carson DA, Salvatore A;
WPI; 1996-020344/02.

Treatment of rheumatoid arthritis - by limiting exposure of immune system to arthritogenic peptide(s).

Example 3; Page 36; 52pp; English.

AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility sequence (see AAR95443 and AAR95444) containing peptides. This sequence corresponds to a region of dnaJ. These sequences are present on arthritogenic proteins and are targeted in this invention as antibody recognition sites. The anti-arthritogenic peptide antibodies that are developed can then be administered to a patient who has RA or who is predisposed to develop RA, to reduce the exposure to arthritogenic peptides. The antibodies are produced and administered in milk. An alternative treatment method comprises the administration of a non-adsorbable antibiotic, together with a RA-beggn bacteria (selected from the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the patient who has RA (or a predisposition to it). Candidates for either of these methods can be screened by detecting an in-vitro cellular immune response to an arthritogenic peptide. The method of the invention allows for the reduction of sensitisation to microbial arthritogenic peptides (such as dnaJ). It also limits the exposure of the systemic immune system of humans to RA arthritogenic peptides present in the gastrointestinal tract

Sequence 14 AA;

Query Match 75.0%; Score 64.5; DB 2; Length 14;
Best Local Similarity 93.3%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 OKRAAYDQYGHAAFE 15
|||||
DB 1 OKRAAYDQY-HAAFE 14
|||||

Search completed: March 7, 2005, 09:54:55
Job time : 160 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 09:58:03 ; Search time 130 Seconds
(without alignments)
40.498 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 246509

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	16	14 US-10-001-938-3	Sequence 3, Appli
2	81	94.2	15	9 US-09-756-983-10	Sequence 10, Appl
3	81	94.2	15	9 US-09-828-574-10	Sequence 10, Appl
4	81	94.2	15	14 US-10-001-938-27	Sequence 27, Appl
5	81	94.2	15	14 US-10-299-540-4	Sequence 4, Appli
6	81	94.2	15	14 US-10-299-184-4	Sequence 4, Appli
7	81	94.2	15	14 US-10-239-313A-444	Sequence 444, App
8	81	94.2	16	14 US-10-239-313A-447	Sequence 11, Appl
9	72	83.7	15	9 US-09-828-574-11	Sequence 5, Appli
10	72	83.7	15	14 US-10-299-540-5	Sequence 5, Appli
11	72	83.7	15	14 US-10-299-184-5	Sequence 5, Appli
12	54	62.8	15	14 US-10-299-540-6	Sequence 6, Appli
13	54	62.8	15	14 US-10-299-184-6	Sequence 6, Appli

14	34	39.5	9	14	US-10-283-423-154	Sequence 154, App
15	34	39.5	9	14	US-10-283-423-155	Sequence 155, App
16	34	39.5	9	14	US-10-283-423-157	Sequence 157, App
17	34	39.5	9	14	US-10-283-423-158	Sequence 158, App
18	34	39.5	9	14	US-10-283-423-159	Sequence 159, App
19	34	39.5	9	14	US-10-213-821-154	Sequence 154, App
20	34	39.5	9	14	US-10-213-821-155	Sequence 155, App
21	34	39.5	9	14	US-10-213-821-157	Sequence 157, App
22	34	39.5	9	14	US-10-213-821-158	Sequence 158, App
23	34	39.5	9	14	US-10-213-821-159	Sequence 159, App
24	34	39.5	9	16	US-10-736-048-154	Sequence 154, App
25	34	39.5	9	16	US-10-736-048-155	Sequence 155, App
26	34	39.5	9	16	US-10-736-048-157	Sequence 157, App
27	34	39.5	9	16	US-10-736-048-158	Sequence 158, App
28	34	39.5	9	16	US-10-736-048-159	Sequence 159, App
29	34	39.5	14	14	US-10-161-959-6	Sequence 6, Appli
30	34	39.5	14	14	US-10-283-423-160	Sequence 160, App
31	34	39.5	14	14	US-10-213-821-160	Sequence 160, App
32	34	39.5	14	16	US-10-736-048-160	Sequence 160, App
33	34	39.5	14	17	US-10-845-407-6	Sequence 6, Appli
34	34	39.5	15	9	US-09-756-983-11	Sequence 11, Appl
35	34	39.5	15	14	US-10-161-959-5	Sequence 5, Appli
36	34	39.5	15	14	US-10-299-540-7	Sequence 7, Appli
37	34	39.5	15	14	US-10-299-540-8	Sequence 8, Appli
38	34	39.5	15	14	US-10-299-184-7	Sequence 7, Appli
39	34	39.5	15	14	US-10-299-184-8	Sequence 8, Appli
40	34	39.5	15	14	US-10-239-313A-443	Sequence 443, App
41	34	39.5	15	17	US-10-845-407-5	Sequence 5, Appli
42	32	37.2	13	15	US-10-089-887-58	Sequence 58, Appl
43	31	36.0	12	16	US-10-884-830-26	Sequence 26, Appl
44	31	36.0	12	16	US-10-884-830-285	Sequence 285, App
45	31	36.0	12	16	US-10-884-830-287	Sequence 287, App

ALIGNMENTS

RESULT 1
US-10-001-938-3
; Sequence 3, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-3

Query Match 100.0%; Score 86; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 2
US-09-756-983-10

; Sequence 10, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJp1 heat shock protein
US-09-756-983-10

Query Match 94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 3

US-09-828-574-10
; Sequence 10, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKEN, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1
; CURRENT APPLICATION NUMBER: US/09/828,574
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: dnaJp1 peptide
US-09-828-574-10

Query Match 94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 4

US-10-001-938-27
; Sequence 27, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-27

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 5

US-10-299-540-4
; Sequence 4, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECT
; TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RA
; TITLE OF INVENTION: ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-540-4

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 6

US-10-299-184-4
; Sequence 4, Application US/10299184

Query Match	94.2%	Score 81;	DB 14;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 6.1e-07;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QKRAAYDQYGHAAFE	15	
Db	1	QKRAAYDQYGHAAFE	15	

RESULT 10
US-10-299-540-5
; Sequence 5, Application US/10299540

Publication No. US20030143238A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
TITLE OF INVENTION: AGAINST ARTHRITIS
TITLE OF INVENTION: ARTHRITIS
FILE REFERENCE: UCSD1370-7
CURRENT APPLICATION NUMBER: US/10/299,540
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 08/618,464
PRIOR FILING DATE: 1996-03-15
PRIOR APPLICATION NUMBER: US 08/246,988
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Mutant dnaJ peptide
US-10-299-540-5

Query Match 83.7%; Score 72; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAPE 15
:|||||
Db 2 ERAAYDQYGHAAPE 15

RESULT 11
US-10-299-184-5
Sequence 5, Application US/10299184
Publication No. US20030147910A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
TITLE OF INVENTION: AGAINST ARTHRITIS
TITLE OF INVENTION: ARTHRITIS
FILE REFERENCE: UCSD1370-6
CURRENT APPLICATION NUMBER: US/10/299,184
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 08/618,464
PRIOR FILING DATE: 1996-03-15
PRIOR APPLICATION NUMBER: US 08/246,988
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Mutant dnaJ peptide
US-10-299-184-5

Query Match 83.7%; Score 72; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAPE 15
:|||||
Db 2 ERAAYDQYGHAAPE 15

RESULT 12
US-10-299-540-6
Sequence 6, Application US/10299540
Publication No. US20030143238A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
TITLE OF INVENTION: AGAINST ARTHRITIS
TITLE OF INVENTION: ARTHRITIS
FILE REFERENCE: UCSD1370-7
CURRENT APPLICATION NUMBER: US/10/299,540
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 08/618,464
PRIOR FILING DATE: 1996-03-15
PRIOR APPLICATION NUMBER: US 08/246,988
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Bacterial dnaJp2 peptide
US-10-299-540-6

Query Match 62.8%; Score 54; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYQ 10
:|||||
Db 6 QKRAAYDQYQ 15

RESULT 13
US-10-299-184-6
Sequence 6, Application US/10299184
Publication No. US20030147910A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
TITLE OF INVENTION: AGAINST ARTHRITIS
TITLE OF INVENTION: ARTHRITIS
FILE REFERENCE: UCSD1370-6
CURRENT APPLICATION NUMBER: US/10/299,184
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 08/618,464
PRIOR FILING DATE: 1996-03-15
PRIOR APPLICATION NUMBER: US 08/246,988
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 15

```
;
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bacterial dnaQp2 peptide
US-10-299-184-6
    Query Match      62.8%; Score 54; DB 14; Length 15;
    Best Local Similarity 100.0%; Pred. No. 0.024;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 QKRAAYDQYG 10
      |||||
Db      6 QKRAAYDQYG 15
      |||||

RESULT 14
US-10-283-423-154
; Sequence 154, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: PHRM0002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-154

    Query Match      39.5%; Score 34; DB 14; Length 9;
    Best Local Similarity 55.6%; Pred. No. 1.3e+06;
    Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY      6 YDOYGHAAF 14
      :|||
Db      1 FDDYGHLPF 9
      :|||

Search completed: March 7, 2005, 10:10:13
Job time : 130 secs

;
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bacterial dnaQp2 peptide
US-10-299-184-6
    Query Match      62.8%; Score 54; DB 14; Length 15;
    Best Local Similarity 100.0%; Pred. No. 0.024;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 QKRAAYDQYG 10
      |||||
Db      6 QKRAAYDQYG 15
      |||||

RESULT 15
US-10-283-423-155
; Sequence 155, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: PHRM0002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-154

    Query Match      39.5%; Score 34; DB 14; Length 9;
    Best Local Similarity 55.6%; Pred. No. 1.3e+06;
    Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY      6 YDOYGHAAF 14
      :|||
Db      1 FDDYGHLPF 9
      :|||

Search completed: March 7, 2005, 10:10:13
Job time : 130 secs
```

This Page Blank (uspio)

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 09:52:27 ; Search time 41 Seconds
(without alignments)
29.131 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAVDQGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 171351

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	94.2	15	1	US-08-618-464-4
2	81	94.2	15	3	US-09-107-615-4
3	81	94.2	15	4	US-09-756-983-10
4	81	94.2	15	5	PCT-US95-04896-4
5	72	83.7	15	1	US-08-618-464-5
6	72	83.7	15	3	US-09-107-615-5
7	72	83.7	15	5	PCT-US95-04896-5
8	54	62.8	15	1	US-08-618-464-6
9	54	62.8	15	3	US-09-107-615-6
10	34	39.5	9	4	US-09-693-746-154
11	34	39.5	9	4	US-09-693-746-155
12	34	39.5	9	4	US-09-693-746-157
13	34	39.5	9	4	US-09-693-746-158
14	34	39.5	9	4	US-09-693-746-159
15	34	39.5	14	4	US-09-693-746-160
16	34	39.5	15	1	US-08-618-464-7
17	34	39.5	15	1	US-08-618-464-8
18	34	39.5	15	3	US-09-107-615-7
19	34	39.5	15	3	US-09-107-615-8
20	34	39.5	15	4	US-09-756-983-11
21	31	36.0	12	1	US-07-732-114A-5
22	31	36.0	12	1	US-08-170-114A-5
23	31	36.0	14	2	US-08-323-686-3
24	31	36.0	14	2	US-08-323-686-26
25	31	36.0	15	4	US-09-255-501-67
26	31	36.0	15	4	US-09-255-501-68
27	31	36.0	15	4	US-09-060-872A-67

28	31	36.0	15	4	US-09-060-872A-68	Sequence 68, Appl
29	31	36.0	15	4	US-09-500-135C-67	Sequence 67, Appl
30	31	36.0	15	4	US-09-500-135C-68	Sequence 68, Appl
31	30	34.9	9	4	US-09-721-870-180	Sequence 180, App
32	30	34.9	15	3	US-08-467-023-255	Sequence 255, App
33	28	32.6	11	3	US-08-467-580-14	Sequence 14, Appl
34	28	32.6	11	5	PCT-US95-08516-14	Sequence 14, Appl
35	28	32.6	15	2	US-08-521-871A-3	Sequence 3, Appl
36	27	31.4	12	1	US-07-732-114A-11	Sequence 11, Appl
37	27	31.4	12	1	US-08-170-114A-11	Sequence 11, Appl
38	27	31.4	13	1	US-08-487-568-45	Sequence 45, Appl
39	26	30.2	6	1	US-07-995-503A-12	Sequence 12, Appl
40	26	30.2	6	1	US-08-390-510-12	Sequence 12, Appl
41	26	30.2	6	1	US-08-390-790-12	Sequence 12, Appl
42	26	30.2	6	2	US-08-390-509-12	Sequence 12, Appl
43	26	30.2	6	3	US-09-149-860A-12	Sequence 12, Appl
44	26	30.2	12	1	US-07-995-503A-11	Sequence 11, Appl
45	26	30.2	12	1	US-08-390-510-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-618-464-4

; Sequence 4, Application US/08618464

; Patent No. 5773570

; GENERAL INFORMATION:

; APPLICANT: CARSON, DENNIS A.

; APPLICANT: ALBANI, SALVATORE

; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN

; TITLE OF INVENTION: INVOLVED IN

; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & RICHARDSON P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CALIFORNIA

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: US/08/618,464

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: HOWELLS, STACY L.

; REGISTRATION NUMBER: 34,842

; REFERENCE/DOCKET NUMBER: 07340/042001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; CLONE: Immucogenic dnaJ Peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..15

US-08-618-464-4

Query Match 94.2% Score 81; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||

RESULT 2

US-09-107-615-4
; Sequence 4, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHROGENIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15

US-09-107-615-4

Query Match 94.2%; Score 81; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||

RESULT 3

US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. 6787154
; GENERAL INFORMATION:
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJp1 heat shock protein
; US-09-756-983-10

Query Match 94.2%; Score 81; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||

RESULT 4

PCT-US95-04896-4
; Sequence 4, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:

US-09-756-983-10

Query Match 94.2%; Score 81; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||

RESULT 5

US-09-107-615-4
; Sequence 4, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHROGENIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15

US-09-107-615-4

Query Match 94.2%; Score 81; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||

RESULT 6

PCT-US95-04896-4
; Sequence 4, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:

US-09-756-983-10

Query Match 94.2%; Score 81; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
Db |||||

RESULT 7

US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. 6787154
; GENERAL INFORMATION:
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJp1 heat shock protein
; US-09-756-983-10

US-09-756-983-10

Query Match 94.2%; Score 81; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US95-04896-4

Query Match 94.2%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 5

US-08-618-464-5
; Sequence 5, Application US/08618464
; Patent No. 5773570

GENERAL INFORMATION:

; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INDUCING
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:

CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; CLONE: Immunogenic dnaJ Peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..15

US-08-618-464-5

Query Match 83.7%; Score 72; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | |
Db 2 ERAAYDQYGHAAFE 15

RESULT 6

US-09-107-615-5
; Sequence 5, Application US/09107615
; Patent No. 6153200

GENERAL INFORMATION:

; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIS
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & RICHARDSON P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CALIFORNIA

; COUNTRY: US

; ZIP: 92037

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/618,464

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: HOWELLS, STACY L.

; REGISTRATION NUMBER: 34,842

; REFERENCE/DOCKET NUMBER: 07340/042001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; CLONE: Immunogenic dnaJ Peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..15

US-09-107-615-5

Query Match 83.7%; Score 72; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | |

Db 2 ERAAYDQYGHAAFE 15
| | | | | | | | | | | | | | | |

RESULT 7

PCT-US95-04896-5

; Sequence 5, Application PC/TUS9504896

GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR

/ CITY: LOS ANGELES
/ STATE: CALIFORNIA
/ COUNTRY: US
/ ZIP: 90012
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/04896
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BERLINER, ROBERT
/ REGISTRATION NUMBER: 20,121
/ REFERENCE/DOCKET NUMBER: 5555-314
/ TELEPHONE: 213-977-1001
/ TELEFAX: 213-977-1003
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ CLONE: Immunogenic dnaJ Peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..15
/ PCT-US95-04896-5

Query Match 83.7%; Score 72; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.le-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 8
US-08-618-464-6
; Sequence 6, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INDUCING IN
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.

/ REGISTRATION NUMBER: 34,842
/ REFERENCE/DOCKET NUMBER: 07340/042001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619/678-5070
/ TELEFAX: 619/678-5099
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ CLONE: dnaJp2
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..15
/ US-08-618-464-6

Query Match 62.8%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
:|||||
Db 6 QKRAAYDQYG 15

RESULT 9
US-09-107-615-6
; Sequence 6, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619/678-5070
/ TELEFAX: 619/678-5099
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide

```
; IMMEDIATE SOURCE:
; CLONE: dnaJp2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-6

Query Match          62.8%; Score 54; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDOYG 10
Db 6 OKRAAYDOYG 15

RESULT 10
US-09-693-746-154
; Sequence 154, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-154

Query Match          39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDOYGHAAF 14
Db 1 FDDYGHLPF 9

RESULT 11
US-09-693-746-155
; Sequence 155, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-155

Query Match          39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDOYGHAAF 14
Db 1 FDDYGHLPF 9

RESULT 12
US-09-693-746-157
; Sequence 157, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-157

Query Match          39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDOYGHAAF 14
Db 1 FDDYGHLPF 9

RESULT 13
US-09-693-746-158
; Sequence 158, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-158
```

```
; IMMEDIATE SOURCE:
; CLONE: dnaJp2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-6

Query Match          39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDOYGHAAF 14
Db 1 FDDYGHLPF 9

RESULT 12
US-09-693-746-157
; Sequence 157, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-157

Query Match          39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDOYGHAAF 14
Db 1 FDDYGHLPF 9

RESULT 13
US-09-693-746-158
; Sequence 158, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; PRIOR FILING DATE: 2000-10-20
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-158
```

Query Match 39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDQYGHAAF 14
: |||||
Db 1 FDDYGHMRF 9

RESULT 14

US-09-693-746-159
; Sequence 159, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.LCD
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-159

Query Match 39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 YDQYGHAAF 14
: |||||
Db 1 FDDYGHMRF 9

RESULT 15

US-09-693-746-160
; Sequence 160, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.LCD
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 160
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-160

Query Match 39.5%; Score 34; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 14;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 6 YDQYGHAAF 14
: |||||
Db 6 FDDYGHMRF 14
Search completed: March 7, 2005, 10:07:26
Job time : 41 secs